

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2004, 10:36:01 ; Search time 53 Seconds  
(without alignments)  
3.753 Million cell updates/sec

Title: US-10-633-913-3

Perfect score: 5444

Sequence: 1 gccccagggccctggagaggt.....aggatcagaagttactac 5444

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 811 seqs, 18271 residues

Total number of hits satisfying chosen parameters: 1622

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 817 summaries

Database : ref3.seq.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.4	0.5	35	1	ACCESSION:BB894837
2	25.4	0.5	36	1	ACCESSION:B1761940
3	25	0.5	34	1	ACCESSION:CF315464
4	25	0.5	35	1	ACCESSION:CO785671
5	24.6	0.5	32	1	ACCESSION:CC887678
6	24.4	0.4	34	1	ACCESSION:AM334249
7	24	0.4	32	1	ACCESSION:AJ791147
8	24	0.4	33	1	ACCESSION:CF334899
9	24	0.4	33	1	ACCESSION:AZ586641
10	23.4	0.4	33	1	ACCESSION:CF291613
11	23.4	0.4	33	1	ACCESSION:CF311229
12	23.4	0.4	33	1	ACCESSION:CF326967
13	23.4	0.4	33	1	ACCESSION:CF328313
14	23.4	0.4	33	1	ACCESSION:CF336752
15	23.4	0.4	33	1	ACCESSION:CF337105
16	23.4	0.4	33	1	ACCESSION:CF337105
17	23.4	0.4	33	1	ACCESSION:AZ486795
18	22.6	0.4	31	1	ACCESSION:AZ627839
19	22.4	0.4	31	1	ACCESSION:AM334249
20	22.4	0.4	32	1	ACCESSION:CF291773
21	22.4	0.4	32	1	ACCESSION:CF293936
22	22.4	0.4	32	1	ACCESSION:CF309233
23	22.4	0.4	32	1	ACCESSION:CF309345
24	22.4	0.4	32	1	ACCESSION:CF313717
25	22.4	0.4	32	1	ACCESSION:CF321046
26	22.4	0.4	32	1	ACCESSION:CF328471
27	22.4	0.4	32	1	ACCESSION:CF331270
28	22.4	0.4	32	1	ACCESSION:CF332296
29	22.4	0.4	32	1	ACCESSION:CF332296
30	22.4	0.4	32	1	ACCESSION:AZ314322
31	22.4	0.4	32	1	ACCESSION:AZ459536
32	22.4	0.4	32	1	ACCESSION:AZ470832
33	22.4	0.4	32	1	ACCESSION:AZ611890
					ACCESSION:AZ778018

34	22.4	0.4	32	1	DR85L21T	ACCESSION:AL986044
35	22.2	0.4	28	1	T56352	ACCESSION:T56352
36	22	0.4	30	1	AZ458127	ACCESSION:AZ458127
37	22	0.4	31	1	BO591372	ACCESSION:BO591372
38	22	0.4	31	1	AZ597046	ACCESSION:AZ597046
39	21.6	0.4	28	1	H68053	ACCESSION:H68053
40	21.6	0.4	29	1	AZ825156	ACCESSION:AZ825156
41	21.6	0.4	30	1	AU267300	ACCESSION:AU267300
42	21.6	0.4	30	1	AZ443322	ACCESSION:AZ443322
43	21	0.4	29	1	CF279536	ACCESSION:CF279536
44	21	0.4	29	1	CF299920	ACCESSION:CF299920
45	21	0.4	29	1	CF312601	ACCESSION:CF312601
46	21	0.4	29	1	CN545237	ACCESSION:CN545237
47	21	0.4	29	1	CN546188	ACCESSION:CN546188
48	21	0.4	29	1	CN546382	ACCESSION:CN546382
49	21	0.4	29	1	CN546438	ACCESSION:CN546438
50	21	0.4	29	1	CN546537	ACCESSION:CN546537
51	21	0.4	29	1	AZ389566	ACCESSION:AZ389566
52	21	0.4	29	1	AZ414283	ACCESSION:AZ414283
53	21	0.4	29	1	AZ451930	ACCESSION:AZ451930
54	21	0.4	29	1	AZ468402	ACCESSION:AZ468402
55	21	0.4	29	1	AZ486793	ACCESSION:AZ486793
56	21	0.4	29	1	AZ661709	ACCESSION:AZ661709
57	21	0.4	29	1	AZ784208	ACCESSION:AZ784208
58	21	0.4	29	1	AZ806470	ACCESSION:AZ806470
59	21	0.4	29	1	AZ812242	ACCESSION:AZ812242
60	21	0.4	29	1	AZ868731	ACCESSION:AZ868731
61	21	0.4	29	1	TA334090	ACCESSION:TA334090
62	21	0.4	29	1	AG193759	ACCESSION:AG193759
63	21	0.4	30	1	AL038650	ACCESSION:AL038650
64	21	0.4	30	1	BG666435	ACCESSION:BG666435
65	21	0.4	30	1	BG665511	ACCESSION:BG665511
66	21	0.4	30	1	CF280699	ACCESSION:CF280699
67	21	0.4	30	1	CF292086	ACCESSION:CF292086
68	21	0.4	30	1	CF299555	ACCESSION:CF299555
69	21	0.4	30	1	CF312417	ACCESSION:CF312417
70	21	0.4	30	1	CF322226	ACCESSION:CF322226
71	21	0.4	30	1	CF327835	ACCESSION:CF327835
72	21	0.4	30	1	CF336555	ACCESSION:CF336555
73	21	0.4	30	1	CN545845	ACCESSION:CN545845
74	21	0.4	30	1	CN545913	ACCESSION:CN545913
75	21	0.4	30	1	CN546459	ACCESSION:CN546459
76	21	0.4	30	1	CN546474	ACCESSION:CN546474
77	21	0.4	30	1	CN546789	ACCESSION:CN546789
78	21	0.4	30	1	AZ357603	ACCESSION:AZ357603
79	21	0.4	30	1	AZ455741	ACCESSION:AZ455741
80	21	0.4	30	1	AZ481739	ACCESSION:AZ481739
81	21	0.4	30	1	AZ582114	ACCESSION:AZ582114
82	21	0.4	30	1	AG191161	ACCESSION:AG191161
83	20.8	0.4	29	1	AU267990	ACCESSION:AU267990
84	20.6	0.4	27	1	AZ941721	ACCESSION:AZ941721
85	20.6	0.4	27	1	AZ970621	ACCESSION:AZ970621
86	20.6	0.4	28	1	CF307749	ACCESSION:CF307749
87	20.6	0.4	28	1	AZ824574	ACCESSION:AZ824574
88	20.6	0.4	28	1	AZ836072	ACCESSION:AZ836072
89	20.6	0.4	29	1	BO583967	ACCESSION:BO583967
90	20.2	0.4	25	1	CF317007	ACCESSION:CF317007
91	20.2	0.4	26	1	AL038686	ACCESSION:AL038686
92	20.2	0.4	26	1	CF299646	ACCESSION:CF299646
93	20.2	0.4	28	1	CF337400	ACCESSION:CF337400
94	20	0.4	28	1	A1971979	ACCESSION:A1971979
95	20	0.4	28	1	AJ666435	ACCESSION:AJ666435
96	20	0.4	28	1	AM332443	ACCESSION:AM332443
97	20	0.4	28	1	CF282351	ACCESSION:CF282351
98	20	0.4	28	1	CF321885	ACCESSION:CF321885
99	20	0.4	28	1	CF330748	ACCESSION:CF330748
100	20	0.4	28	1	CF330938	ACCESSION:CF330938
101	20	0.4	28	1	CN546364	ACCESSION:CN546364
102	20	0.4	28	1	CN546703	ACCESSION:CN546703
103	20	0.4	28	1	AZ399637	ACCESSION:AZ399637
104	20	0.4	28	1	AZ401766	ACCESSION:AZ401766
105	20	0.4	28	1	AZ471744	ACCESSION:AZ471744
106	20	0.4	28	1	AZ493138	ACCESSION:AZ493138

C 107	20	0.4	28 1	A2653365	ACCESSION: A2653365	180	18.2	0.3	23 1	CP334657	ACCESSION: CP334657
C 108	20	0.4	28 1	A2785035	ACCESSION: A2785035	C 181	18.2	0.3	23 1	CN545540	ACCESSION: CN545540
C 109	20	0.4	28 1	A2824519	ACCESSION: A2824519	C 182	18.2	0.3	23 1	CN546520	ACCESSION: CN546520
C 110	20	0.4	28 1	A2833425	ACCESSION: A2833425	C 183	18.2	0.3	23 1	COS77495	ACCESSION: COS77495
C 111	20	0.4	28 1	A2866569	ACCESSION: A2866569	C 184	18.2	0.3	23 1	A2309219	ACCESSION: A2309219
C 112	20	0.4	28 1	TA291A01Q	ACCESSION: AL486613	C 185	18.2	0.3	23 1	A2309851	ACCESSION: A2309851
C 113	20	0.4	28 1	TA291A09P	ACCESSION: AL453073	C 186	18.2	0.3	23 1	A2312214	ACCESSION: A2312214
C 114	20	0.4	28 1	TA379D11P	ACCESSION: AL497637	C 187	18.2	0.3	23 1	A2313922	ACCESSION: A2313922
C 115	19.8	0.4	25 1	BG929133	ACCESSION: BG929133	C 188	18.2	0.3	23 1	A2351354	ACCESSION: A2351354
C 116	19.8	0.4	27 1	CD028815	ACCESSION: CD028815	C 189	18.2	0.3	23 1	A2357645	ACCESSION: A2357645
C 117	19.8	0.4	27 1	CT654516	ACCESSION: CT654516	C 190	18.2	0.3	23 1	A2419236	ACCESSION: A2419236
C 118	19.6	0.4	27 1	A2776487	ACCESSION: A2776487	C 191	18.2	0.3	23 1	A2461220	ACCESSION: A2461220
C 119	19.6	0.4	27 1	A2862643	ACCESSION: A2862643	C 192	18.2	0.3	23 1	A2465327	ACCESSION: A2465327
C 120	19.6	0.4	27 1	A2873739	ACCESSION: A2873739	C 193	18.2	0.3	23 1	A2481702	ACCESSION: A2481702
C 121	19.6	0.4	27 1	TA257807P	ACCESSION: AL483278	C 194	18.2	0.3	23 1	A2588254	ACCESSION: A2588254
C 122	19.4	0.4	23 1	A2430288	ACCESSION: A2430288	C 195	18.2	0.3	23 1	A2593540	ACCESSION: A2593540
C 123	19.2	0.4	25 1	AL587648	ACCESSION: AL587648	C 196	18.2	0.3	23 1	A2610785	ACCESSION: A2610785
C 124	19.2	0.4	25 1	A2381039	ACCESSION: A2381039	C 197	18.2	0.3	23 1	A2647637	ACCESSION: A2647637
C 125	19.2	0.4	25 1	A2386891	ACCESSION: A2386891	C 198	18.2	0.3	23 1	A2654903	ACCESSION: A2654903
C 126	19.2	0.4	26 1	AL587774	ACCESSION: AL587774	C 199	18.2	0.3	23 1	A2787851	ACCESSION: A2787851
C 127	19.2	0.4	26 1	R26779	ACCESSION: R26779	C 200	18.2	0.3	23 1	A2792751	ACCESSION: A2792751
C 128	19	0.3	27 1	AM327923	ACCESSION: AM327923	C 201	18.2	0.3	23 1	A2859570	ACCESSION: A2859570
C 129	19	0.3	27 1	CP291968	ACCESSION: CP291968	C 202	18.2	0.3	23 1	A2939608	ACCESSION: A2939608
C 130	19	0.3	27 1	CP288811	ACCESSION: CP288811	C 203	18.2	0.3	23 1	BH000534	ACCESSION: BH000534
C 131	19	0.3	27 1	CP29725	ACCESSION: CP29725	C 204	18.2	0.3	23 1	TA151C02Q	ACCESSION: AL473028
C 132	19	0.3	27 1	CP330557	ACCESSION: CP330557	C 205	18.2	0.3	23 1	TA274B03P	ACCESSION: AL484584
C 133	19	0.3	27 1	CP335229	ACCESSION: CP335229	C 206	18.2	0.3	23 1	TA353A10P	ACCESSION: AL494456
C 134	19	0.3	27 1	CN545326	ACCESSION: CN545326	C 207	18.2	0.3	23 1	AM247159	ACCESSION: AM247159
C 135	19	0.3	27 1	CN545492	ACCESSION: CN545492	C 208	18.2	0.3	24 1	BG670391	ACCESSION: BG670391
C 136	19	0.3	27 1	CN545530	ACCESSION: CN545530	C 209	18.2	0.3	24 1	BX554611	ACCESSION: BX554611
C 137	19	0.3	27 1	CN545597	ACCESSION: CN545597	C 210	18.2	0.3	24 1	CP276855	ACCESSION: CP276855
C 138	19	0.3	27 1	CN545938	ACCESSION: CN545938	C 211	18.2	0.3	24 1	CP281313	ACCESSION: CP281313
C 139	19	0.3	27 1	CN545962	ACCESSION: CN545962	C 212	18.2	0.3	24 1	CP301561	ACCESSION: CP301561
C 140	19	0.3	27 1	CN546052	ACCESSION: CN546052	C 213	18.2	0.3	24 1	CP320862	ACCESSION: CP320862
C 141	19	0.3	27 1	CN546271	ACCESSION: CN546271	C 214	18.2	0.3	24 1	CN545249	ACCESSION: CN545249
C 142	19	0.3	27 1	CN546337	ACCESSION: CN546337	C 215	18.2	0.3	24 1	CN545307	ACCESSION: CN545307
C 143	19	0.3	27 1	CN546559	ACCESSION: CN546559	C 216	18.2	0.3	24 1	CN545657	ACCESSION: CN545657
C 144	19	0.3	27 1	CN546574	ACCESSION: CN546574	C 217	18.2	0.3	24 1	CN545784	ACCESSION: CN545784
C 145	19	0.3	27 1	N89936	ACCESSION: N89936	C 218	18.2	0.3	24 1	CN546689	ACCESSION: CN546689
C 146	19	0.3	27 1	A2344642	ACCESSION: A2344642	C 219	18.2	0.3	24 1	A2328848	ACCESSION: A2328848
C 147	19	0.3	27 1	A2401672	ACCESSION: A2401672	C 220	18.2	0.3	24 1	A2328652	ACCESSION: A2328652
C 148	19	0.3	27 1	A2434285	ACCESSION: A2434285	C 221	18.2	0.3	24 1	A2386491	ACCESSION: A2386491
C 149	19	0.3	27 1	A2458228	ACCESSION: A2458228	C 222	18.2	0.3	24 1	A2390642	ACCESSION: A2390642
C 150	19	0.3	27 1	A2486791	ACCESSION: A2486791	C 223	18.2	0.3	24 1	A2438069	ACCESSION: A2438069
C 151	19	0.3	27 1	A2495352	ACCESSION: A2495352	C 224	18.2	0.3	24 1	A2458112	ACCESSION: A2458112
C 152	19	0.3	27 1	A2511894	ACCESSION: A2511894	C 225	18.2	0.3	24 1	A2459280	ACCESSION: A2459280
C 153	19	0.3	27 1	A2580921	ACCESSION: A2580921	C 226	18.2	0.3	24 1	A2621257	ACCESSION: A2621257
C 154	19	0.3	27 1	A2616094	ACCESSION: A2616094	C 227	18.2	0.3	24 1	A2644621	ACCESSION: A2644621
C 155	19	0.3	27 1	A2623186	ACCESSION: A2623186	C 228	18.2	0.3	24 1	A2786257	ACCESSION: A2786257
C 156	19	0.3	27 1	A2627847	ACCESSION: A2627847	C 229	18.2	0.3	24 1	A2834990	ACCESSION: A2834990
C 157	19	0.3	27 1	A2809295	ACCESSION: A2809295	C 230	18.2	0.3	24 1	A2970038	ACCESSION: A2970038
C 158	19	0.3	27 1	TA355B06P	ACCESSION: AL493923	C 231	18.2	0.3	24 1	A2984490	ACCESSION: A2984490
C 159	18.8	0.3	23 1	A2382013	ACCESSION: A2382013	C 232	18.2	0.3	24 1	A2993423	ACCESSION: A2993423
C 160	18.8	0.3	24 1	CD743368	ACCESSION: CD743368	C 233	18.2	0.3	24 1	TA169D12P	ACCESSION: AL478922
C 161	18.8	0.3	25 1	A2404078	ACCESSION: A2404078	C 234	18.2	0.3	24 1	TA27B08Q	ACCESSION: AL453584
C 162	18.8	0.3	26 1	A2316353	ACCESSION: A2316353	C 235	18.2	0.3	24 1	TA354C06P	ACCESSION: AL494439
C 163	18.6	0.3	26 1	A2813253	ACCESSION: A2813253	C 236	18.2	0.3	24 1	TA371E11P	ACCESSION: AL495622
C 164	18.6	0.3	25 1	CP638767	ACCESSION: CP638767	C 237	18.2	0.3	24 1	TA95808P	ACCESSION: AL459003
C 165	18.6	0.3	25 1	M59260	ACCESSION: M59260	C 238	18.2	0.3	24 1	AU265663	ACCESSION: AU265663
C 166	18.6	0.3	26 1	A2355083	ACCESSION: A2355083	C 239	18.2	0.3	25 1	CP291048	ACCESSION: CP291048
C 167	18.6	0.3	26 1	A2337459	ACCESSION: A2337459	C 240	18.2	0.3	25 1	CP291646	ACCESSION: CP291646
C 168	18.6	0.3	26 1	A2623156	ACCESSION: A2623156	C 241	18.2	0.3	25 1	CP299288	ACCESSION: CP299288
C 169	18.6	0.3	26 1	AG201580	ACCESSION: AG201580	C 242	18.2	0.3	25 1	CP300333	ACCESSION: CP300333
C 170	18.4	0.3	22 1	A2464354	ACCESSION: A2464354	C 243	18.2	0.3	25 1	CP301712	ACCESSION: CP301712
C 171	18.2	0.3	23 1	AJ695799	ACCESSION: AJ695799	C 244	18.2	0.3	25 1	CP316323	ACCESSION: CP316323
C 172	18.2	0.3	23 1	AJ747297	ACCESSION: AJ747297	C 245	18.2	0.3	25 1	CP317714	ACCESSION: CP317714
C 173	18.2	0.3	23 1	CP279238	ACCESSION: CP279238	C 246	18.2	0.3	25 1	CP319073	ACCESSION: CP319073
C 174	18.2	0.3	23 1	CP297943	ACCESSION: CP297943	C 247	18.2	0.3	25 1	CP330786	ACCESSION: CP330786
C 175	18.2	0.3	23 1	CP310501	ACCESSION: CP310501	C 248	18.2	0.3	25 1	CN545505	ACCESSION: CN545505
C 176	18.2	0.3	23 1	CP319212	ACCESSION: CP319212	C 249	18.2	0.3	25 1	CN546041	ACCESSION: CN546041
C 177	18.2	0.3	23 1	CP322953	ACCESSION: CP322953	C 250	18.2	0.3	25 1	CN546397	ACCESSION: CN546397
C 178	18.2	0.3	23 1	CP329042	ACCESSION: CP329042	C 251	18.2	0.3	25 1	CN546477	ACCESSION: CN546477
C 179	18.2	0.3	23 1	CP329694	ACCESSION: CP329694	C 252	18.2	0.3	25 1		

C 253	18.2	0.3	25	1	CN546728	ACCESSION:CN546728	326	17.2	0.3	22	1	AJ747407	ACCESSION:AJ747407
C 254	18.2	0.3	25	1	N33150	ACCESSION:N33150	327	17.2	0.3	22	1	AL038477	ACCESSION:AL038477
C 255	18.2	0.3	25	1	AZ344725	ACCESSION:AZ344725	328	17.2	0.3	22	1	AM332181	ACCESSION:AM332181
C 256	18.2	0.3	25	1	AZ350777	ACCESSION:AZ350777	329	17.2	0.3	22	1	AM332399	ACCESSION:AM332399
C 257	18.2	0.3	25	1	AZ389458	ACCESSION:AZ389458	330	17.2	0.3	22	1	CF299342	ACCESSION:CF299342
C 258	18.2	0.3	25	1	AZ609234	ACCESSION:AZ609234	331	17.2	0.3	22	1	CF300133	ACCESSION:CF300133
C 259	18.2	0.3	25	1	AZ623157	ACCESSION:AZ623157	332	17.2	0.3	22	1	CF311036	ACCESSION:CF311036
C 260	18.2	0.3	25	1	AZ788646	ACCESSION:AZ788646	333	17.2	0.3	22	1	CF311269	ACCESSION:CF311269
C 261	18.2	0.3	25	1	AZ832800	ACCESSION:AZ832800	334	17.2	0.3	22	1	CF311713	ACCESSION:CF311713
C 262	18.2	0.3	25	1	AZ949287	ACCESSION:AZ949287	335	17.2	0.3	22	1	CF312498	ACCESSION:CF312498
C 263	18.2	0.3	25	1	AZ980407	ACCESSION:AZ980407	336	17.2	0.3	22	1	CF330679	ACCESSION:CF330679
C 264	18.2	0.3	25	1	AL42971	ACCESSION:AL42971	337	17.2	0.3	22	1	CF333430	ACCESSION:CF333430
C 265	18.2	0.3	25	1	TA324E10P	ACCESSION:TA324E10P	338	17.2	0.3	22	1	CF334781	ACCESSION:CF334781
C 266	18.2	0.3	26	1	AJ659204	ACCESSION:AJ659204	339	17.2	0.3	22	1	CF336250	ACCESSION:CF336250
C 267	18.2	0.3	26	1	AM37613	ACCESSION:AM37613	340	17.2	0.3	22	1	CF337580	ACCESSION:CF337580
C 268	18.2	0.3	26	1	BM658913	ACCESSION:BM658913	341	17.2	0.3	22	1	CF338524	ACCESSION:CF338524
C 269	18.2	0.3	26	1	BX563414	ACCESSION:BX563414	342	17.2	0.3	22	1	CN545550	ACCESSION:CN545550
C 270	18.2	0.3	26	1	CF278359	ACCESSION:CF278359	343	17.2	0.3	22	1	AZ310066	ACCESSION:AZ310066
C 271	18.2	0.3	26	1	CF282426	ACCESSION:CF282426	344	17.2	0.3	22	1	AZ351527	ACCESSION:AZ351527
C 272	18.2	0.3	26	1	CF296851	ACCESSION:CF296851	345	17.2	0.3	22	1	AZ357630	ACCESSION:AZ357630
C 273	18.2	0.3	26	1	CF297087	ACCESSION:CF297087	346	17.2	0.3	22	1	AZ388103	ACCESSION:AZ388103
C 274	18.2	0.3	26	1	CF299701	ACCESSION:CF299701	347	17.2	0.3	22	1	AZ401908	ACCESSION:AZ401908
C 275	18.2	0.3	26	1	CF302874	ACCESSION:CF302874	348	17.2	0.3	22	1	AZ424307	ACCESSION:AZ424307
C 276	18.2	0.3	26	1	CF311369	ACCESSION:CF311369	349	17.2	0.3	22	1	AZ428818	ACCESSION:AZ428818
C 277	18.2	0.3	26	1	CF331439	ACCESSION:CF331439	350	17.2	0.3	22	1	AZ442146	ACCESSION:AZ442146
C 278	18.2	0.3	26	1	CF337311	ACCESSION:CF337311	351	17.2	0.3	22	1	AZ459654	ACCESSION:AZ459654
C 279	18.2	0.3	26	1	CN545213	ACCESSION:CN545213	352	17.2	0.3	22	1	AZ463503	ACCESSION:AZ463503
C 280	18.2	0.3	26	1	CN545225	ACCESSION:CN545225	353	17.2	0.3	22	1	AZ463652	ACCESSION:AZ463652
C 281	18.2	0.3	26	1	CN545546	ACCESSION:CN545546	354	17.2	0.3	22	1	AZ582403	ACCESSION:AZ582403
C 282	18.2	0.3	26	1	CN545723	ACCESSION:CN545723	355	17.2	0.3	22	1	AZ607658	ACCESSION:AZ607658
C 283	18.2	0.3	26	1	CN545888	ACCESSION:CN545888	356	17.2	0.3	22	1	AZ654691	ACCESSION:AZ654691
C 284	18.2	0.3	26	1	CN546608	ACCESSION:CN546608	357	17.2	0.3	22	1	AZ760533	ACCESSION:AZ760533
C 285	18.2	0.3	26	1	CN546649	ACCESSION:CN546649	358	17.2	0.3	22	1	AZ779844	ACCESSION:AZ779844
C 286	18.2	0.3	26	1	AZ342914	ACCESSION:AZ342914	359	17.2	0.3	22	1	AZ785019	ACCESSION:AZ785019
C 287	18.2	0.3	26	1	AZ359871	ACCESSION:AZ359871	360	17.2	0.3	22	1	AZ787098	ACCESSION:AZ787098
C 288	18.2	0.3	26	1	AZ376664	ACCESSION:AZ376664	361	17.2	0.3	22	1	AZ787606	ACCESSION:AZ787606
C 289	18.2	0.3	26	1	AZ389765	ACCESSION:AZ389765	362	17.2	0.3	22	1	AZ792704	ACCESSION:AZ792704
C 290	18.2	0.3	26	1	AZ414673	ACCESSION:AZ414673	363	17.2	0.3	22	1	TA31B09P	ACCESSION:TA31B09P
C 291	18.2	0.3	26	1	AZ593300	ACCESSION:AZ593300	364	17.2	0.3	22	1	TA329P10P	ACCESSION:TA329P10P
C 292	18.2	0.3	26	1	AZ612722	ACCESSION:AZ612722	365	17.2	0.3	22	1	AZ810674	ACCESSION:AZ810674
C 293	18.2	0.3	26	1	AZ624441	ACCESSION:AZ624441	366	17.2	0.3	22	1	AZ841661	ACCESSION:AZ841661
C 294	18.2	0.3	26	1	AZ627846	ACCESSION:AZ627846	367	17.2	0.3	22	1	AZ843514	ACCESSION:AZ843514
C 295	18.2	0.3	26	1	AZ635695	ACCESSION:AZ635695	368	17.2	0.3	22	1	AZ846164	ACCESSION:AZ846164
C 296	18.2	0.3	26	1	AZ652515	ACCESSION:AZ652515	369	17.2	0.3	22	1	TA329P10P	ACCESSION:TA329P10P
C 297	18.2	0.3	26	1	AZ800453	ACCESSION:AZ800453	370	17.2	0.3	22	1	TA35C120P	ACCESSION:TA35C120P
C 298	18.2	0.3	26	1	AZ963974	ACCESSION:AZ963974	371	17.2	0.3	22	1	TA380A07P	ACCESSION:TA380A07P
C 299	18.2	0.3	26	1	TA324D07P	ACCESSION:TA324D07P	372	17.2	0.3	22	1	AG194579	ACCESSION:AG194579
C 300	17.8	0.3	21	1	BX548564	ACCESSION:BX548564	373	17.2	0.3	23	1	AL038397	ACCESSION:AL038397
C 301	17.8	0.3	21	1	AZ394897	ACCESSION:AZ394897	374	17.2	0.3	23	1	AL038592	ACCESSION:AL038592
C 302	17.8	0.3	21	1	AZ486776	ACCESSION:AZ486776	375	17.2	0.3	23	1	AL038609	ACCESSION:AL038609
C 303	17.8	0.3	21	1	AZ589098	ACCESSION:AZ589098	376	17.2	0.3	23	1	AL038668	ACCESSION:AL038668
C 304	17.8	0.3	21	1	AZ597932	ACCESSION:AZ597932	377	17.2	0.3	23	1	CF300172	ACCESSION:CF300172
C 305	17.8	0.3	21	1	AZ627978	ACCESSION:AZ627978	378	17.2	0.3	23	1	CF332379	ACCESSION:CF332379
C 306	17.8	0.3	21	1	AZ828285	ACCESSION:AZ828285	379	17.2	0.3	23	1	AZ425710	ACCESSION:AZ425710
C 307	17.8	0.3	22	1	AZ633751	ACCESSION:AZ633751	380	17.2	0.3	23	1	AZ447220	ACCESSION:AZ447220
C 308	17.8	0.3	22	1	AZ892888	ACCESSION:AZ892888	381	17.2	0.3	23	1	AZ801003	ACCESSION:AZ801003
C 309	17.8	0.3	24	1	AZ627850	ACCESSION:AZ627850	382	17.2	0.3	23	1	AZ973926	ACCESSION:AZ973926
C 310	17.8	0.3	25	1	AU247142	ACCESSION:AU247142	383	17.2	0.3	24	1	TA55C06P	ACCESSION:TA55C06P
C 311	17.8	0.3	25	1	CD028814	ACCESSION:CD028814	384	17.2	0.3	24	1	CA853764	ACCESSION:CA853764
C 312	17.8	0.3	25	1	AZ510124	ACCESSION:AZ510124	385	17.2	0.3	24	1	CF312319	ACCESSION:CF312319
C 313	17.8	0.3	25	1	AZ659095	ACCESSION:AZ659095	386	17.2	0.3	24	1	AZ781101	ACCESSION:AZ781101
C 314	17.8	0.3	25	1	AZ664804	ACCESSION:AZ664804	387	17.2	0.3	24	1	AZ812579	ACCESSION:AZ812579
C 315	17.6	0.3	24	1	AZ396663	ACCESSION:AZ396663	388	16.8	0.3	23	1	CF296213	ACCESSION:CF296213
C 316	17.6	0.3	24	1	AZ514388	ACCESSION:AZ514388	389	16.8	0.3	23	1	AL587602	ACCESSION:AL587602
C 317	17.6	0.3	24	1	AZ607198	ACCESSION:AZ607198	390	16.6	0.3	23	1	CF297907	ACCESSION:CF297907
C 318	17.6	0.3	24	1	AZ626101	ACCESSION:AZ626101	391	16.6	0.3	23	1	CF334077	ACCESSION:CF334077
C 319	17.6	0.3	24	1	AZ814559	ACCESSION:AZ814559	392	16.6	0.3	23	1	AZ486853	ACCESSION:AZ486853
C 320	17.6	0.3	25	1	AZ330737	ACCESSION:AZ330737	393	16.6	0.3	23	1	AZ627841	ACCESSION:AZ627841
C 321	17.4	0.3	19	1	AZ510952	ACCESSION:AZ510952	394	16.6	0.3	23	1	AZ452554	ACCESSION:AZ452554
C 322	17.4	0.3	20	1	AZ433566	ACCESSION:AZ433566	395	16.6	0.3	23	1	AZ970753	ACCESSION:AZ970753
C 323	17.4	0.3	20	1	AZ492997	ACCESSION:AZ492997	396	16.6	0.3	23	1	CL693171	ACCESSION:CL693171
C 324	17.4	0.3	20	1	AZ770557	ACCESSION:AZ770557	397	16.4	0.3	19	1	AZ489586	ACCESSION:AZ489586
C 325	17.4	0.3	22	1	AJ649983	ACCESSION:AJ649983	398	16.4	0.3	19	1	AZ983014	ACCESSION:AZ983014

C 399	16.4	0.3	23	1	AZ333204	ACCESSION:AZ333204	472	15.8	0.3	20	1	AZ75620	ACCESSION:AZ75620
C 400	16.2	0.3	21	1	AJ658282	ACCESSION:AJ658282	473	15.8	0.3	20	1	AZ94997	ACCESSION:AZ94997
C 401	16.2	0.3	21	1	AJ666203	ACCESSION:AJ666203	C 474	15.8	0.3	21	1	AZ445540	ACCESSION:AZ445540
C 402	16.2	0.3	21	1	AL048777	ACCESSION:AL048777	C 475	15.8	0.3	22	1	TA28D010	ACCESSION:AL453252
C 403	16.2	0.3	21	1	CF282216	ACCESSION:CF282216	C 476	15.6	0.3	22	1	AZ454585	ACCESSION:AZ345485
C 404	16.2	0.3	21	1	CF292703	ACCESSION:CF292703	C 477	15.6	0.3	22	1	AZ785081	ACCESSION:AZ785081
C 405	16.2	0.3	21	1	CF295642	ACCESSION:CF295642	C 478	15.6	0.3	22	1	BH000233	ACCESSION:BH000233
C 406	16.2	0.3	21	1	CF297615	ACCESSION:CF297615	C 479	15.4	0.3	18	1	BQ594437	ACCESSION:BQ594437
C 407	16.2	0.3	21	1	CF298322	ACCESSION:CF298322	C 480	15.4	0.3	19	1	CL436223	ACCESSION:CL436223
C 408	16.2	0.3	21	1	CF300809	ACCESSION:CF300809	C 481	15.4	0.3	11	1	AZ308846	ACCESSION:AZ308846
C 409	16.2	0.3	21	1	CF312715	ACCESSION:CF312715	C 482	15.4	0.3	21	1	AB094448	ACCESSION:AB094448
C 410	16.2	0.3	21	1	CF316073	ACCESSION:CF316073	C 483	15.4	0.3	22	1	AJ666402	ACCESSION:AJ666402
C 411	16.2	0.3	21	1	CF326952	ACCESSION:CF326952	C 484	15.2	0.3	20	1	AL038427	ACCESSION:AL038427
C 412	16.2	0.3	21	1	CF327391	ACCESSION:CF327391	C 485	15.2	0.3	20	1	AL038429	ACCESSION:AL038429
C 413	16.2	0.3	21	1	CF332956	ACCESSION:CF332956	C 486	15.2	0.3	20	1	AL038507	ACCESSION:AL038507
C 414	16.2	0.3	21	1	CF338057	ACCESSION:CF338057	C 487	15.2	0.3	20	1	AL038570	ACCESSION:AL038570
C 415	16.2	0.3	21	1	CF338552	ACCESSION:CF338552	C 488	15.2	0.3	20	1	AL038576	ACCESSION:AL038576
C 416	16.2	0.3	21	1	CN546469	ACCESSION:CN546469	C 489	15.2	0.3	20	1	AL038750	ACCESSION:AL038750
C 417	16.2	0.3	21	1	CN546504	ACCESSION:CN546504	C 490	15.2	0.3	20	1	AL038754	ACCESSION:AL038754
C 418	16.2	0.3	21	1	CN546595	ACCESSION:CN546595	C 491	15.2	0.3	20	1	AL038845	ACCESSION:AL038845
C 419	16.2	0.3	21	1	CO779794	ACCESSION:CO779794	C 492	15.2	0.3	20	1	AL587630	ACCESSION:AL587630
C 420	16.2	0.3	21	1	AZ317208	ACCESSION:AZ317208	C 493	15.2	0.3	20	1	AM334823	ACCESSION:AM334823
C 421	16.2	0.3	21	1	AZ348593	ACCESSION:AZ348593	C 494	15.2	0.3	20	1	CP280913	ACCESSION:CP280913
C 422	16.2	0.3	21	1	AZ350611	ACCESSION:AZ350611	C 495	15.2	0.3	20	1	CP282035	ACCESSION:CP282035
C 423	16.2	0.3	21	1	AZ386711	ACCESSION:AZ386711	C 496	15.2	0.3	20	1	CP282414	ACCESSION:CP282414
C 424	16.2	0.3	21	1	AZ386794	ACCESSION:AZ386794	C 497	15.2	0.3	20	1	CP282418	ACCESSION:CP282418
C 425	16.2	0.3	21	1	AZ389287	ACCESSION:AZ389287	C 498	15.2	0.3	20	1	CP298018	ACCESSION:CP298018
C 426	16.2	0.3	21	1	AZ389687	ACCESSION:AZ389687	C 499	15.2	0.3	20	1	CF299822	ACCESSION:CF299822
C 427	16.2	0.3	21	1	AZ406936	ACCESSION:AZ406936	C 500	15.2	0.3	20	1	CF301720	ACCESSION:CF301720
C 428	16.2	0.3	21	1	AZ412739	ACCESSION:AZ412739	C 501	15.2	0.3	20	1	CF302027	ACCESSION:CF302027
C 429	16.2	0.3	21	1	AZ412951	ACCESSION:AZ412951	C 502	15.2	0.3	20	1	CF308984	ACCESSION:CF308984
C 430	16.2	0.3	21	1	AZ415029	ACCESSION:AZ415029	C 503	15.2	0.3	20	1	CF310604	ACCESSION:CF310604
C 431	16.2	0.3	21	1	AZ465890	ACCESSION:AZ465890	C 504	15.2	0.3	20	1	CF313067	ACCESSION:CF313067
C 432	16.2	0.3	21	1	AZ611116	ACCESSION:AZ611116	C 505	15.2	0.3	20	1	CF313569	ACCESSION:CF313569
C 433	16.2	0.3	21	1	AZ611423	ACCESSION:AZ611423	C 506	15.2	0.3	20	1	CF319133	ACCESSION:CF319133
C 434	16.2	0.3	21	1	AZ615628	ACCESSION:AZ615628	C 507	15.2	0.3	20	1	CF321721	ACCESSION:CF321721
C 435	16.2	0.3	21	1	AZ627843	ACCESSION:AZ627843	C 508	15.2	0.3	20	1	CP328565	ACCESSION:CP328565
C 436	16.2	0.3	21	1	AZ627845	ACCESSION:AZ627845	C 509	15.2	0.3	20	1	CP333173	ACCESSION:CP333173
C 437	16.2	0.3	21	1	AZ657727	ACCESSION:AZ657727	C 510	15.2	0.3	20	1	CP334170	ACCESSION:CP334170
C 438	16.2	0.3	21	1	AZ766552	ACCESSION:AZ766552	C 511	15.2	0.3	20	1	CP336525	ACCESSION:CP336525
C 439	16.2	0.3	21	1	AZ769976	ACCESSION:AZ769976	C 512	15.2	0.3	20	1	CP337494	ACCESSION:CP337494
C 440	16.2	0.3	21	1	AZ792613	ACCESSION:AZ792613	C 513	15.2	0.3	20	1	CN545446	ACCESSION:CN545446
C 441	16.2	0.3	21	1	AZ793486	ACCESSION:AZ793486	C 514	15.2	0.3	20	1	CN545501	ACCESSION:CN545501
C 442	16.2	0.3	21	1	AZ799327	ACCESSION:AZ799327	C 515	15.2	0.3	20	1	TS0579	ACCESSION:TS0579
C 443	16.2	0.3	21	1	AZ810054	ACCESSION:AZ810054	C 516	15.2	0.3	20	1	AZ333980	ACCESSION:AZ333980
C 444	16.2	0.3	21	1	AZ815424	ACCESSION:AZ815424	C 517	15.2	0.3	20	1	AZ337671	ACCESSION:AZ337671
C 445	16.2	0.3	21	1	AZ819181	ACCESSION:AZ819181	C 518	15.2	0.3	20	1	AZ341237	ACCESSION:AZ341237
C 446	16.2	0.3	21	1	AZ821218	ACCESSION:AZ821218	C 519	15.2	0.3	20	1	AZ341530	ACCESSION:AZ341530
C 447	16.2	0.3	21	1	AZ843603	ACCESSION:AZ843603	C 520	15.2	0.3	20	1	AZ343031	ACCESSION:AZ343031
C 448	16.2	0.3	21	1	AZ853429	ACCESSION:AZ853429	C 521	15.2	0.3	20	1	AZ343730	ACCESSION:AZ343730
C 449	16.2	0.3	21	1	AZ960063	ACCESSION:AZ960063	C 522	15.2	0.3	20	1	AZ351273	ACCESSION:AZ351273
C 450	16.2	0.3	21	1	BH000837	ACCESSION:BH000837	C 523	15.2	0.3	20	1	AZ357623	ACCESSION:AZ357623
C 451	16.2	0.3	22	1	CF282024	ACCESSION:CF282024	C 524	15.2	0.3	20	1	AZ369734	ACCESSION:AZ369734
C 452	16.2	0.3	22	1	CF298427	ACCESSION:CF298427	C 525	15.2	0.3	20	1	AZ386573	ACCESSION:AZ386573
C 453	16.2	0.3	22	1	CF310486	ACCESSION:CF310486	C 526	15.2	0.3	20	1	AZ396481	ACCESSION:AZ396481
C 454	16.2	0.3	22	1	CO778290	ACCESSION:CO778290	C 527	15.2	0.3	20	1	AZ405596	ACCESSION:AZ405596
C 455	16.2	0.3	22	1	AZ304806	ACCESSION:AZ304806	C 528	15.2	0.3	20	1	AZ442328	ACCESSION:AZ442328
C 456	16.2	0.3	22	1	AZ374487	ACCESSION:AZ374487	C 529	15.2	0.3	20	1	AZ463331	ACCESSION:AZ463331
C 457	16.2	0.3	22	1	AZ505769	ACCESSION:AZ505769	C 530	15.2	0.3	20	1	AZ477734	ACCESSION:AZ477734
C 458	16.2	0.3	22	1	AZ823875	ACCESSION:AZ823875	C 531	15.2	0.3	20	1	AZ479464	ACCESSION:AZ479464
C 459	16.2	0.3	22	1	AZ845735	ACCESSION:AZ845735	C 532	15.2	0.3	20	1	AZ486784	ACCESSION:AZ486784
C 460	16.2	0.3	22	1	TA303G05P	ACCESSION:TA303G05P	C 533	15.2	0.3	20	1	AZ486787	ACCESSION:AZ486787
C 461	16.2	0.3	22	1	AL048776	ACCESSION:AL048776	C 534	15.2	0.3	20	1	AZ498625	ACCESSION:AZ498625
C 462	16.2	0.3	23	1	AL0487621	ACCESSION:AL0487621	C 535	15.2	0.3	20	1	AZ514729	ACCESSION:AZ514729
C 463	16.2	0.3	23	1	BQ590647	ACCESSION:BQ590647	C 536	15.2	0.3	20	1	AZ579122	ACCESSION:AZ579122
C 464	16.2	0.3	23	1	BX559898	ACCESSION:BX559898	C 537	15.2	0.3	20	1	AZ579178	ACCESSION:AZ579178
C 465	16.2	0.3	23	1	CF279593	ACCESSION:CF279593	C 538	15.2	0.3	20	1	AZ581208	ACCESSION:AZ581208
C 466	16.2	0.3	23	1	AZ621676	ACCESSION:AZ621676	C 539	15.2	0.3	20	1	AZ588011	ACCESSION:AZ588011
C 467	16.2	0.3	23	1	AZ817623	ACCESSION:AZ817623	C 540	15.2	0.3	20	1	AZ607328	ACCESSION:AZ607328
C 468	16.2	0.3	23	1	AI371092	ACCESSION:AI371092	C 541	15.2	0.3	20	1	AZ623155	ACCESSION:AZ623155
C 469	15.8	0.3	19	1	AZ654747	ACCESSION:AZ654747	C 542	15.2	0.3	20	1	AZ623214	ACCESSION:AZ623214
C 470	15.8	0.3	19	1	CL693177	ACCESSION:CL693177	C 543	15.2	0.3	20	1	AZ643992	ACCESSION:AZ643992
C 471	15.8	0.3	19	1			C 544	15.2	0.3	20	1	AZ645829	ACCESSION:AZ645829



545	15.2	0.3	20	1	AZ650271	ACCESSION:AZ650271	C 618	14.2	0.3	19	1	CF298472	ACCESSION:CF298472
546	15.2	0.3	20	1	AZ760838	ACCESSION:AZ760838	C 619	14.2	0.3	19	1	CF299598	ACCESSION:CF299598
547	15.2	0.3	20	1	AZ764504	ACCESSION:AZ764504	C 620	14.2	0.3	19	1	CF300236	ACCESSION:CF300236
548	15.2	0.3	20	1	AZ755211	ACCESSION:AZ755211	C 621	14.2	0.3	19	1	CF302327	ACCESSION:CF302327
549	15.2	0.3	20	1	AZ772091	ACCESSION:AZ772091	C 622	14.2	0.3	19	1	CF302456	ACCESSION:CF302456
550	15.2	0.3	20	1	AZ779425	ACCESSION:AZ779425	C 623	14.2	0.3	19	1	CF304589	ACCESSION:CF304589
551	15.2	0.3	20	1	AZ784041	ACCESSION:AZ784041	C 624	14.2	0.3	19	1	CF309636	ACCESSION:CF309636
552	15.2	0.3	20	1	AZ793467	ACCESSION:AZ793467	C 625	14.2	0.3	19	1	CF309801	ACCESSION:CF309801
553	15.2	0.3	20	1	AZ798529	ACCESSION:AZ798529	C 626	14.2	0.3	19	1	CF309943	ACCESSION:CF309943
554	15.2	0.3	20	1	AZ805163	ACCESSION:AZ805163	C 627	14.2	0.3	19	1	CF311496	ACCESSION:CF311496
555	15.2	0.3	20	1	AZ806521	ACCESSION:AZ806521	C 628	14.2	0.3	19	1	CF311513	ACCESSION:CF311513
556	15.2	0.3	20	1	AZ806585	ACCESSION:AZ806585	C 629	14.2	0.3	19	1	CF312403	ACCESSION:CF312403
557	15.2	0.3	20	1	AZ809306	ACCESSION:AZ809306	C 630	14.2	0.3	19	1	CF315299	ACCESSION:CF315299
558	15.2	0.3	20	1	AZ810986	ACCESSION:AZ810986	C 631	14.2	0.3	19	1	CF316480	ACCESSION:CF316480
559	15.2	0.3	20	1	AZ813908	ACCESSION:AZ813908	C 632	14.2	0.3	19	1	CF318788	ACCESSION:CF318788
560	15.2	0.3	20	1	AZ817323	ACCESSION:AZ817323	C 633	14.2	0.3	19	1	CF329136	ACCESSION:CF329136
561	15.2	0.3	20	1	AZ817414	ACCESSION:AZ817414	C 634	14.2	0.3	19	1	CF329137	ACCESSION:CF329137
562	15.2	0.3	20	1	AZ817467	ACCESSION:AZ817467	C 635	14.2	0.3	19	1	CF329986	ACCESSION:CF329986
563	15.2	0.3	20	1	AZ818489	ACCESSION:AZ818489	C 636	14.2	0.3	19	1	CF332063	ACCESSION:CF332063
564	15.2	0.3	20	1	AZ818816	ACCESSION:AZ818816	C 637	14.2	0.3	19	1	CF333507	ACCESSION:CF333507
565	15.2	0.3	20	1	AZ818816	ACCESSION:AZ818816	C 638	14.2	0.3	19	1	CF333753	ACCESSION:CF333753
566	15.2	0.3	20	1	AZ837491	ACCESSION:AZ837491	C 639	14.2	0.3	19	1	CF334014	ACCESSION:CF334014
567	15.2	0.3	20	1	AZ841342	ACCESSION:AZ841342	C 640	14.2	0.3	19	1	CN545602	ACCESSION:CN545602
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571	15.2	0.3	20	1	AZ858419	ACCESSION:AZ858419	C 644	14.2	0.3	19	1	AZ307313	ACCESSION:AZ307313
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573	15.2	0.3	20	1	AZ949180	ACCESSION:AZ949180	C 646	14.2	0.3	19	1	AZ310105	ACCESSION:AZ310105
574	15.2	0.3	20	1	AZ963973	ACCESSION:AZ963973	C 647	14.2	0.3	19	1	AZ317743	ACCESSION:AZ317743
575	15.2	0.3	20	1	AL0380297	ACCESSION:AL0380297	C 648	14.2	0.3	19	1	AZ340311	ACCESSION:AZ340311
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578	15.2	0.3	21	1	AL587702	ACCESSION:AL587702	C 651	14.2	0.3	19	1	AZ364226	ACCESSION:AZ364226
579	15.2	0.3	21	1	BX556006	ACCESSION:BX556006	C 652	14.2	0.3	19	1	AZ365696	ACCESSION:AZ365696
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584	15.2	0.3	21	1	CF319122	ACCESSION:CF319122	C 657	14.2	0.3	19	1	AZ410050	ACCESSION:AZ410050
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587	15.2	0.3	21	1	AZ493766	ACCESSION:AZ493766	C 660	14.2	0.3	19	1	AZ424716	ACCESSION:AZ424716
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594	14.8	0.3	19	1	AZ650252	ACCESSION:AZ650252	C 667	14.2	0.3	19	1	AZ486786	ACCESSION:AZ486786
595	14.8	0.3	19	1	AZ650575	ACCESSION:AZ650575	C 668	14.2	0.3	19	1	AZ490652	ACCESSION:AZ490652
596	14.8	0.3	19	1	AZ766990	ACCESSION:AZ766990	C 669	14.2	0.3	19	1	AZ508040	ACCESSION:AZ508040
597	14.8	0.3	20	1	AM333777	ACCESSION:AM333777	C 670	14.2	0.3	19	1	AZ509929	ACCESSION:AZ509929
598	14.8	0.3	20	1	CN754148	ACCESSION:CN754148	C 671	14.2	0.3	19	1	AZ579119	ACCESSION:AZ579119
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601	14.8	0.3	21	1	AZ602152	ACCESSION:AZ602152	C 674	14.2	0.3	19	1	AZ593210	ACCESSION:AZ593210
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604	14.8	0.3	21	1	AZ764492	ACCESSION:AZ764492	C 677	14.2	0.3	19	1	AZ631701	ACCESSION:AZ631701
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606	14.8	0.3	21	1	CL693188	ACCESSION:CL693188	C 679	14.2	0.3	19	1	AZ643659	ACCESSION:AZ643659
607	14.4	0.3	19	1	AZ353907	ACCESSION:AZ353907	C 680	14.2	0.3	19	1	AZ644698	ACCESSION:AZ644698
608	14.4	0.3	19	1	AJ954509	ACCESSION:AJ954509	C 681	14.2	0.3	19	1	AZ645841	ACCESSION:AZ645841
609	14.2	0.3	19	1	AJ666205	ACCESSION:AJ666205	C 682	14.2	0.3	19	1	AZ648335	ACCESSION:AZ648335
610	14.2	0.3	19	1	AJ666179	ACCESSION:AJ666179	C 683	14.2	0.3	19	1	AZ649888	ACCESSION:AZ649888
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616	14.2	0.3	19	1	CF291090	ACCESSION:CF291090	C 689	14.2	0.3	19	1	AZ778858	ACCESSION:AZ778858
617	14.2	0.3	19	1	CF298396	ACCESSION:CF298396	C 690	14.2	0.3	19	1	AZ779901	ACCESSION:AZ779901

691	14.2	0.3	19	1	ACCESSION: A2781876	691	14.2	0.3	19	1	ACCESSION: CF329484	691	14.2	0.3	19	1	ACCESSION: CF329485	691	14.2	0.3	19	1	ACCESSION: CF329486
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700	14.2	0.3	19	1	ACCESSION: A2841581	700	14.2	0.3	19	1	ACCESSION: CF329511	700	14.2	0.3	19	1	ACCESSION: CF329512	700	14.2	0.3	19	1	ACCESSION: CF329513
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703	14.2	0.3	19	1	ACCESSION: A2936798	703	14.2	0.3	19	1	ACCESSION: CF329520	703	14.2	0.3	19	1	ACCESSION: CF329521	703	14.2	0.3	19	1	ACCESSION: CF329522
704	14.2	0.3	19	1	ACCESSION: A2962226	704	14.2	0.3	19	1	ACCESSION: CF329523	704	14.2	0.3	19	1	ACCESSION: CF329524	704	14.2	0.3	19	1	ACCESSION: CF329525
705	14.2	0.3	19	1	ACCESSION: A2985501	705	14.2	0.3	19	1	ACCESSION: CF329526	705	14.2	0.3	19	1	ACCESSION: CF329527	705	14.2	0.3	19	1	ACCESSION: CF329528
706	14.2	0.3	19	1	ACCESSION: BH000498	706	14.2	0.3	19	1	ACCESSION: CF329529	706	14.2	0.3	19	1	ACCESSION: CF329530	706	14.2	0.3	19	1	ACCESSION: CF329531
707	14.2	0.3	19	1	ACCESSION: A2600883	707	14.2	0.3	19	1	ACCESSION: CF329532	707	14.2	0.3	19	1	ACCESSION: CF329533	707	14.2	0.3	19	1	ACCESSION: CF329534
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709	14.2	0.3	19	1	ACCESSION: CL685439	709	14.2	0.3	19	1	ACCESSION: CF329538	709											

RESULT	1
BE894837	
LOCUS	
DEFINITION	BE894837 35 bp mRNA linear EST 20-OCT-2000 601424018F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919061 5', mRNA sequence.
ACCESSION	BE894837
VERSION	BE894837
KEYWORDS	BE894837.1 GI:10357627
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 35) NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
REFERENCE	
AUTHORS	

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.llnl.gov

Plate: LIM9748 row: d column: 06  
High quality sequence start: 4  
High quality sequence stop: 35.  
Location/Qualifiers

## FEATURES

source

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/clone="IMAGE:3919061"  
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/lab\_host="DH10B (phage-resistant)"  
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Query Match 0.5%; Score 25.4; DB 1; Length 35;  
Best Local Similarity 82.9%; Pred. No. 33;  
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5390 ATTAATAATACAAAAAGAAAAATGAAATTA 5424  
|||||  
1 ATTAATAATACAAAAAGAAAAATGAAATTA 35

RESULT 2  
LOCUS B1761940 36 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603048772F1 NIH\_MGC\_116 Homo sapiens CDNA clone IMAGE:5189224 5',  
mRNA sequence.

ACCESSION B1761940  
VERSION B1761940.1 GI:15753518  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 36)  
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.llnl.gov  
Plate: LIM91472 row: o column: 17  
High quality sequence stop: 36.  
Location/Qualifiers

## FEATURES

source

1.36  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5189224"  
/lab\_host="DH10B"  
/note="Organ: pooled colon, kidney, stomach; Vector:

pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 clones, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH-MGC Library."

Query Match 0.5%; Score 25.4; DB 1; Length 36;  
Best Local Similarity 82.9%; Pred. No. 34;  
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTAAGG 5427  
|||||  
1 AAAAAATACAAAAAGAAAAATGAAATTAAGG 35

RESULT 3  
LOCUS CF315464/c 34 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD-04-G09.b1 OSHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) CDNA clone HD-04-G09, mRNA sequence.

ACCESSION CF315464  
VERSION CF315464.1 GI:33687225  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Bukaryova; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriaroidae; Oryzaceae; Oryza.  
1 (bases 1 to 34)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1.34  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="RNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
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/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 25; DB 1; Length 34;  
Best Local Similarity 84.8%; Pred. No. 36;  
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTA 5425  
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Db 33 AAAAAATACAAAAAGAAAAATGAAATTA 1

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RESULT 4
LOCUS      CO785671/c      35 bp      mRNA      linear      EST 05-AUG-2004
DEFINITION BL284A_H08 6-Day Axiolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
            cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION  CO785671
VERSION     CO785671.1  GI:51001651
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
ORGANISM    Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroides; Ambystomatidae;
            Ambystoma.
REFERENCE   1 (bases 1 to 35)
AUTHORS     Habermann, B., Behn, A.G., Herklotz, S., Volkmers, M., Eckelt, K.,
            Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, R.M.
TITLE       An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating Blastema
            cDNA libraries
JOURNAL     Genome Biol. (2004) In press
COMMENT     Tanaka lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pflaenauerstrasse 108, 01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL284A row: 08 column: H
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
            source
            1..35
            /organism="Ambystoma mexicanum"
            /mol_type="mRNA"
            /db_xref="taxon:8296"
            /tissue_type="Tail Blastema"
            /cell_type="regenerating tail blastema"
            /clone_lib="6-Day Axiolotl Tail Blastema (6DAXBL)"
            /note="Vector: PCWVSPORT6; Site 1: NotI; Site 2: SalI;
            Unnormalized cDNA plasmid library prepared by Invitrogen.
            Size fractionated mRNA was polyA+ primed and cloned into
            NotI-SalI site of PCWVSPORT6. Bacterial host is
            EMDH10B-TONA. Average insert size is 1.67 kb.
            TAG_LIB=6DAXBL"

Query Match      0.5%; Score 25; DB 1; Length 35;
Best Local Similarity 84.8%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5393 AAAAAATACAAAAAGAAAAATGAAATATA 5425
      1 ||||| ||||| ||||| ||||| ||||| |||||
      23 AAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAA 1

RESULT 5
LOCUS      CC887678      32 bp      DNA      linear      GSS 31-JUL-2003
DEFINITION SALK_150577.31.20 x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_150577.31.20.X, genomic
            survey sequence.
ACCESSION  CC887678
VERSION     CC887678
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
            Gadinah, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
            Shin, P., Zimmermann, J. and Ecker, U.R.
TITLE       A Sequence-Indexed Library of Insertion Mutations in the

```

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JOURNAL     Arabidopsis Genome
COMMENT     Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At2g10590.
            Class: TDNA tagged.
FEATURES
            source
            1..32
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone_lib="SALK_150577.31.20.X"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"

Query Match      0.5%; Score 24.6; DB 1; Length 32;
Best Local Similarity 87.1%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3981 CATCAAGCTGAGCCTGAGCTGTGGAAGCT 4011
      1 ||||| ||||| ||||| ||||| ||||| |||||
      2 CTTGAAGTCTGAGCTGAGTGTGGAAGCT 32

RESULT 6
LOCUS      AM334249/c      34 bp      mRNA      linear      EST 31-JAN-2000
DEFINITION S32P4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AM334249
VERSION     AM334249.1  GI:6830606
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1 (bases 1 to 34)
AUTHORS     Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
            Edman, J.C., Kovacs, J. and Cushion, M.
TITLE       Expressed sequence tags from Pneumocystis carinii
JOURNAL     Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES
            source
            1..34
            /organism="Pneumocystis carinii"
            /mol_type="mRNA"
            /db_xref="taxon:4754"
            /lab_host="E. coli"
            /clone_lib="AGS-1"
            /note="Vector: Lambda Zap II; Site 1: EcoRI; Site 2: XhoI;
            P. carinii organisms (3x10es) from a single rat (99-1-6,
            sacrificed on 3/17/99) at Cincinnati VA facilities.
            Trizol extracted RNA. Oligo dT priming, standard
            conditions described by vendor, Stratagene. Further
            details see www.uky.edu/Project/Pneumocystis/"

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Query Match 0.4%; Score 24.4; DB 1; Length 34;  
 Best Local Similarity 82.4%; Pred. No. 43;  
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5382 ATTGAAGATTAAAAATGCAAAAAAGAAAAA 5415  
 |||||  
 34 ATTAAAAAAGAAAAAAGAAAAA 1

RESULT 7  
 AJ791147/c 32 bp mRNA linear EST 09-AUG-2004  
 LOCUS AJ791147 Antirrhinum majus whole plant Antirrhinum majus cDNA clone  
 DEFINITION 018.2.07.001, mRNA sequence.

ACCESSION AJ791147.1 GI:51061240  
 VERSION AJ791147.1  
 KEYWORDS EST.  
 SOURCE Antirrhinum majus (snapdragon)  
 ORGANISM Antirrhinum majus

REFERENCE 1 (bases 1 to 32)  
 Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.  
 Antirrhinum EST collection  
 TITLE Antirrhinum EST collection  
 JOURNAL Unpublished (2003)

COMMENT Contact: Schwarz-Sommer Z.  
 Molekulare Pflanzen-genetik  
 MPI fuer Zuechtungs-forschung  
 Carl-von-Linne Weg 10, D-50829, Germany.  
 Location/Qualifiers

## FEATURES

source  
 1..32  
 /organism="Antirrhinum majus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4151"  
 /clone="018.2.07.001"  
 /issue\_type="Whole plant"  
 /clone\_lib="Antirrhinum majus whole plant"

Query Match 0.4%; Score 24; DB 1; Length 32;  
 Best Local Similarity 84.4%; Pred. No. 45;  
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5394 AAAAAATACAAAAAAGAAAAATGAAAAATGAA 5425  
 |||||  
 32 AAAAAAAGAAAAAAGAAAAAAGAAAAA 1

RESULT 8  
 CF334899 33 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF334899/c  
 DEFINITION JMT--04-F19.g1 AtCMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-F19, mRNA sequence.  
 ACCESSION CF334899.1 GI:33818141  
 VERSION CF334899.1  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 33)  
 Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,  
 Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of BioScience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

0.4%  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

## FEATURES

## source

1..33  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39847"  
 /clone="JMT--04-F19"  
 /issue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ATCMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana (Jasmonate Carboxyl methyltransferase overexpression line.)"

Query Match 0.4%; Score 24; DB 1; Length 33;  
 Best Local Similarity 84.4%; Pred. No. 47;  
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5394 AAAAAATACAAAAAAGAAAAATGAAAAATGAA 5425  
 |||||  
 33 AAAAAAAGAAAAAAGAAAAAAGAAAAA 2

## RESULT 9

AZ586641 33 bp DNA linear GSS 13-DEC-2000  
 LOCUS AZ586641  
 DEFINITION 1M0392N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0392N08 R, genomic survey sequence.  
 ACCESSION AZ586641  
 VERSION AZ586641.1 GI:11708831  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 33)  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Iselm, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Iselm, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymer Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0392 row: N column: 08  
 Seq primer: CACACAGAAACAGCATATGAC  
 class: plasmid ends  
 High quality sequence stop: 33.  
 Location/Qualifiers

## FEATURES

## source

1..33  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0392N08"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv, Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|9b|AF129072.1), a copy-number inducible derivative of Plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 24; DB 1; Length 33;  
Best Local Similarity 84.4%; Pred. No. 47;  
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5384 TTAAGATTAAAAATACAAAAAGAAAAA 5415  
DB 2 TTAATATATTAATAAAAAATTTAAAAAGAAAAA 33

RESULT 10  
CF291613/c 33 bp mRNA linear EST 14-AUG-2003  
LOCUS 14R00T--02-B21.b1 Rice root plasmid cDNA library (14R00T) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 14R00T--02-B21, mRNA  
sequence.  
ACCESSION CF291613  
VERSION CF291613.1 GI:33660646  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 33)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..33  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiVar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14R00T--02-B21"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14R00T)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 23.4; DB 1; Length 33;  
Best Local Similarity 81.8%; Pred. No. 56;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAAAATATA 5425  
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11  
CF311229/c 33 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABF--06-F23, mRNA sequence.  
ACCESSION CF311229  
VERSION CF311229.1 GI:33682990  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 33)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..33  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiVar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF--06-F23"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABF-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.4%; Score 23.4; DB 1; Length 33;  
Best Local Similarity 81.8%; Pred. No. 56;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAAAATATA 5425  
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 12  
CF326967/c 33 bp mRNA linear EST 18-AUG-2003  
LOCUS NAC1--01-B04.b1 Rice callus plasmid cDNA library (NAC1) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone NAC1--01-B04, mRNA  
sequence.  
ACCESSION CF326967  
VERSION CF326967.1 GI:33802189  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 33)

Query Match 0.4%; Score 23.4; DB 1; Length 33;  
Best Local Similarity 81.8%; Pred. No. 56;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.

## FEATURES

**Bourse**

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="NACL--01-E04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.4%	Score 23.4;	DB 1;	Length 33;
Best Local Similarity	81.8%;	Pred. No. 56;		
Matches 27; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

5393 AAAAAAAAAAGAAAAATGAATAAA 5425

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13	CF328313	LOCUS	DEFINITION
	CF328313	33 bp	mRNA
			linear
			EST 18-AUG-2003
			NACL--03-C14.g1 Rice callus plasmid cdna library (NACL) Oryza

ACCESSION	CP328313
VERSION	CP328313.1
KEYWORDS	GI:33804873
SOURCE	EST
ORGANISM	<i>Oryza sativa</i> [japonica cultivar-group]
	<i>Oryza sativa</i> [japonica cultivar-group]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 33)	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahn, B.H.	Large-scale Sequencing Analysis of Rice ESTs	Unpublished (2003)	Contact: Nahn B.H.

```

FEATURES      Location/Qualifiers
Source        1. .33

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with oligoribonucleotides and then used as templates for RT-PCR. "

Query Match	0.4%	Score 23.4	DB 1	length 33
Best Local Similarity	81.8%	Pred. No. 56		
Matches 27; Conservative	0	Mismatches 6	Indels 0	Gaps 0

5393 AAAAAAATACAAAAAAGAAAAAATGAAAAATAAA 5423

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 14				
CP336752/c				
LOCUS	CP336752	33 bp	mRNA	linear
DEFINITION	JM-06-019.g1	AtUMT-overexpressing transgenic rice	plasmid cDNA	EST 18-AUG-2003

ACCESSION	CF336752
VERSION	CF336752.1
VERSION	GI:33821884
VERSION	RefSeq

## REFERENCE

TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B. H.

Fax: 82 31 321 6355  
Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr)

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source
1. .33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="TMT-06-019"
/tissue_type="leaf"

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/dev stages="14 days after germination"
/lab host="B.colli DH10B"
/clone lib="ACTUWT-overexpressing transgenic rice plasmid"
/cdna library "(JMT)"
/notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis jasmonate Carboxyl methyltransferase overexpression line."

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Query Match	0.4%	Score 23.4	DB 1	Length 33
Best Local Similarity	81.8%	Pred. No. 56		
Matches	27	Conservative	0	Mismatches 6
				Indels 0
				Gaps 0
QY	5393	AAAAAAAAACGAAAAAAAAACGAAATATA	5425	
DB	33	AAAAAAAAAAAAAAAAAAAAAAAAA	1	

RESULT 15	
CF337105/c	
LOCUS	33 bp mRNA linear
DEFINITION	JMW-07-G18.b1 AtJMW-overexpressing transgenic rice plasmid cDNA library (JMW) Oryza sativa (japonica cultivar-group) cDNA clone JMW-07-G18, mRNA sequence.
ACCESSION	CF337105
VERSION	CF337105.1
KEYWORDS	GI:33822596
	EST.

**SOURCE**  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)

**ORGANISM**  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriocaridaceae; Oryzaceae; Oryza.

**REFERENCE**  
1 (bases 1 to 33)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

**TITLE**  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**COMMENTS**  
Location/Qualifiers

**FEATURES**  
source  
1..33  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="UMT--07-G18"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1ib="AtUMT-overexpressing transgenic rice plasmid  
cDNA library (UMT)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

**Query Match**  
Best Local Similarity 0.4%; Score 23.4; DB 1; Length 33;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

**Db**  
5393 AAAAAAAAAAAGAAAAATGAAAAATAA 5425  
33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

**RESULT 16**  
AZ486795/c 33 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0315P22 Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
DEFINITION clone UUGCLM0315P22 F, genomic survey sequence.  
ACCESSION AZ486795  
VERSION AZ486795.1 GI:10653918  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 33)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: P column: 22

**JOURNAL**  
**COMMENT**

**FEATURES**  
source  
1..33  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0315P22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/nares/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (914732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.4%; Score 23.4; DB 1; Length 33;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

**Db**  
5393 AAAAAAAAAAAGAAAAATGAAAAATAA 5425  
33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

**RESULT 17**  
AZ627839/c 33 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0474B02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
DEFINITION clone UUGCLM0474B02 F, genomic survey sequence.  
ACCESSION AZ627839  
VERSION AZ627839.1 GI:11750125  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 33)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: B column: 02  
Seq primer: CGTGTAAACGACGCGCAGT

**JOURNAL**  
**COMMENT**



Class: plasmid ends  
High quality sequence stop: 33.  
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/clone\_1ib="Mouse 10kb plasmid UGCM library"  
/note="Vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 23.4; DB 1; Length 33;  
Best Local Similarity 81.8%; Pred. No. 56;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTA 5425  
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 18  
LOCUS AU268044 31 bp mRNA linear EST 26-APR-2004  
DEFINITION AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA  
sequence.  
ACCESSION AU268044  
VERSION AU268044  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, B., Ochiai, H., Maeda, M., Williams, J. G., Takeuchi, I. and Tanaka, Y.  
TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium discoideum  
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
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/organism="Dictyostelium discoideum"  
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/db\_xref="taxon:44689"  
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/sex="mat A"

/dev\_stage="vegetative"  
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Query Match 0.4%; Score 22.6; DB 1; Length 31;  
Best Local Similarity 86.2%; Pred. No. 65;  
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5397 AATATCAAAAAAGAAAAATGAAATTA 5425  
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 19  
LOCUS AM327277 32 bp mRNA linear EST 28-JAN-2000  
DEFINITION AM327277 x1 NIH\_MGC\_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA  
sequence.  
ACCESSION AM327277  
VERSION AM327277  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 32)  
AUTHORS NIH-MGC http://mgs.ncl.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Edge Biosystems  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Plate: L1C00028 row: G column: 13  
Seq primer: -21M13 forward primer (ABI).  
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/clone\_1ib="NIH\_MGC\_2"  
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

#### FEATURES

source

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
Best Local Similarity 81.2%; Pred. No. 72;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTA 5424  
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 20  
LOCUS CF291773/c 32 bp mRNA linear EST 14-AUG-2003  
DEFINITION CF291773 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (Japanica cultivar-group) cDNA clone 14ROOT--02-F12, mRNA  
sequence.  
ACCESSION CF291773  
VERSION CF291773  
KEYWORDS EST.  
SOURCE Oryza sativa (Japanica cultivar-group)  
ORGANISM Oryza sativa (Japanica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 32)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
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 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21  
 CF299386/c 32 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-G07, mRNA  
 sequence.  
 ACCESSION CF299386  
 VERSION CF299386  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
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 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 22  
 CF309233 32 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--03-F14, mRNA sequence.  
 ACCESSION CF309233  
 VERSION CF309233  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 /dev\_stage="14 days after germination"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
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 then used for PCR. mRNA was prepared from ABF-responsive  
 element binding transcription factor 3 overexpression  
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Query Match 0.4%; Score 22.4; DB 1; Length 32;  
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 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424  
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RESULT 23  
 CF309345 32 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--03-I03, mRNA sequence.

ACCESSION CP309345 GI:33681106  
 VERSION EST.  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC., DIVISION OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
 Best Local Similarity 81.2%; Pred. No. 72;  
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OR 5393 AAAAAATACAAAAAGAAAAATGAATAA 5424  
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 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 24  
 CP313717/c  
 LOCUS 32 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD-01-P05.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-01-P05, mRNA sequence.

ACCESSION CP313717 GI:33685478  
 VERSION EST.  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC., DIVISION OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
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OR 5393 AAAAAATACAAAAAGAAAAATGAATAA 5424  
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 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 25  
 CP321046/c  
 LOCUS 32 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD-12-C15.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-12-C15, mRNA sequence.

ACCESSION CP321046 GI:33692807  
 VERSION EST.  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 32)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC., DIVISION OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Query Match 0.4%; Score 22.4; DB 1; Length 32;  
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 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 26
CF328471/c 32 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--03-G09, mRNA
sequence.
ACCESSION CF328471 GI:33805189
VERSION CF328471
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarctidae; Oryzaceae; Oryza.
1 (bases 1 to 32)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 27
CF331270/c 32 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--07-F08, mRNA
sequence.
ACCESSION CF331270
VERSION CF331270
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarctidae; Oryzaceae; Oryza.
1 (bases 1 to 32)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS
```

```

TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAAGAAAAATGAAAAATA 5424
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Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 28
CF332296/c 32 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-M01.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-M01, mRNA
sequence.
ACCESSION CF332296
VERSION CF332296
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarctidae; Oryzaceae; Oryza.
1 (bases 1 to 32)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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            /lab_host="E.coli DH10B"
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            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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## RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
 Best Local Similarity 81.2%; Pred. No. 72;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5383 TTTAAGATTATTAATAAATAAGAAAAA 5414  
 |||||  
 32 TTTCAGAAAAAATTAATAAATAAATAA 1

RESULT 29  
 AZ314322 32 bp DNA linear GSS 29-SEP-2000  
 LOCUS AZ314322/c  
 DEFINITION 1M0031IN05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0031IN05 F, genomic survey sequence.

ACCESSION AZ314322  
 VERSION AZ314322.1 GI:10360096

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: N column: 05

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0031IN05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;

Best Local Similarity 81.2%; Pred. No. 72;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAAAAATGAATAATAA 5425  
 |||||  
 32 AAAAAAATCAAAAAAATGAATAATAA 1

RESULT 30  
 AZ459536 32 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ459536/c  
 DEFINITION 1M0264M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0264M16 F, genomic survey sequence.

ACCESSION AZ459536  
 VERSION AZ459536.1 GI:10617577

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0264 row: M column: 16

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0264M16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
Best Local Similarity 81.2%; Pred. No. 72;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAAGAAAAATGAATTA 5424  
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 31  
AZ470832 32 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0285F14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG1M0285F14 F, genomic survey sequence.  
ACCESSION AZ470832  
VERSION AZ470832.1 GI:10628957  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0285 row: F column: 14  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 32.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
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10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.4%; Score 22.4; DB 1; Length 32;

Best Local Similarity 81.2%; Pred. No. 72;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAAGAAAAATGAATTA 5424  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 32  
AZ611890 32 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0438E02R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG1M0438E02 R, genomic survey sequence.  
ACCESSION AZ611890  
VERSION AZ611890.1 GI:11734080  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0438 row: E column: 02  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 32.  
Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

0.4%; Score 22.4; DB 1; Length 32;  
Best Local Similarity 81.2%; Pred. No. 72;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAAAATTA 5424  
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 33  
 A2778018 32 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0012020R Mouse 10kb plasmid UGCM library Mus musculus genomic  
 DEFINITION clone UGCM2M0012020 R, genomic survey sequence.  
 A2778018  
 VERSION A2778018  
 KEYWORDS A2778018.1 GI:12307220  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)

REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weis  
 COMMENT University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0012 row: 0 column: 20  
 Seq primer: CACACAGGAACACGCTATGAC  
 Class: plasmid ends  
 High quality sequence stop: 32.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="UGCM2M0012020"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCM library"  
 /note="Vector: FMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g[4732114]gb|AF12072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
 Best Local Similarity 81.2%; Pred. No. 72;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAAAATTA 5424  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 34  
 DR85L21T 32 bp DNA linear GSS 22-NOV-2002  
 LOCUS Danto rerio genomic clone DKEX-85L21, genomic survey sequence.  
 DEFINITION AL986044  
 ACCESSION AL986044.1 GI:25187956  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Danto rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 32)

REFERENCE  
 AUTHORS Humphray, S.J., Huckle, B. and Hunt, S.E.  
 Direct Submision  
 Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome  
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
 humquerry@sanger.ac.uk Unpublished  
 This sequence was generated from the T7 end of BAC 85L21. 85L21 is  
 part of the Dantokey BAC library created by R. Plaetzer and N.V.  
 Keygene.  
 Further details: http://www.sanger.ac.uk/Projects/D\_rerio/  
 Location/Qualifiers  
 1..32  
 /organism="Danto rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEX-85L21"  
 /issue\_type="Testis"  
 /note="vector pindigoBAC-536"

Query Match 0.4%; Score 22.4; DB 1; Length 32;  
 Best Local Similarity 81.2%; Pred. No. 72;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAAAATTA 5424  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 35  
 T56352 28 bp mRNA linear EST 06-FEB-1995  
 LOCUS yb34c09.g1 Stratagene fetal spleen (#937205) Homo sapiens cDNA  
 DEFINITION clone IMAGE:73072.3, similar to gb:541458.RD  
 CIMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN),  
 mRNA sequence.  
 T56352  
 ACCESSION T56352.1 GI:658213  
 VERSION EST.  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 28)

REFERENCE  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chiappelli, B.,  
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, W., Le, M., Le, N.,  
 Maritz, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,  
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,  
 Trevisan, R., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
 and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags

TITLE JOURNAL MEDLINE PUBMED  
 GENOME RES. 6 (9), 807-828 (1996)  
 97044478  
 8889549  
 COMMENT Contact: Wilson RK

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewartson.wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: -21m13  
 High quality sequence stop: 1.

## FEATURES

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/mol_type="mRNA"
/db_xref="GDB:494737"
/db_xref="taxon:9606"
/clone="IMAGE:73072"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/notes="Organ: spleen; Vector: pBluescript SK-; Site: 1;
ECORI; Site 2: XhoI; Cloned unidirectionally.
Oligo dr. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG
3' -3' adaptor sequence: 5' CTCAGATTGTTTTTTTTTTT 3'"
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Query Match 0.4%; Score 22.2; DB 1; Length 28;  
 Best Local Similarity 85.7%; Pred. No. 65;  
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5394 AAAAAATACAAAAAGAAAAATGAAAA 5421

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 36  
 AZ458127/c 30 bp DNA linear GSS 04-OCT-2000  
 LOCUS  
 DEFINITION  
 1M0261124R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0261124 R, genomic survey sequence.

ACCESSION  
 AZ458127  
 AZ458127.1 GI:10616252

## KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 Class: plasmid ends  
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 Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UGCG1M library"  

/notes="Vector: pMD42nv; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA  

was hydrodynamically sheared by repeated passage through a  

0.005 inch orifice at constant velocity. The sheared DNA  

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polynucleotide kinase. Adaptor oligonucleotides were  

ligated to the blunt ends in high molar excess. The  

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10.5 kb range using preparative agarose gel  

electrophoresis. Vector DNA was prepared from a derivative  

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  

inducible derivative of plasmid R1. The vector was ligated  

with adaptors complementary to the insert adaptors and  

purified. The sheared, adaptor mouse DNA was annealed to  

adaptor vector DNA, and transformed into  

chemically-competent E. coli XL10-Gold (Stratagene) cells  

and selected for ampicillin resistance."
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Query Match 0.4%; Score 22; DB 1; Length 30;  
 Best Local Similarity 83.3%; Pred. No. 75;  
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAATGAAAAATTA 5424

Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 37  
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 LOCUS  
 DEFINITION  
 E012712-024-017-115-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 CDNA clone 024-017-115 3-PRIME, mRNA sequence.

ACCESSION  
 B0591372  
 B0591372.1 GI:26120955

## KEYWORDS

SOURCE

ORGANISM

Beta vulgaris  
 Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp1z-koeln.mpg.de  
 Insert Length: 31 Std Error: 0.00  
 Place: 17 row: 1 column: 15  
 Seq primer: T7; GTAATACGATCTCATATGAGGC.  
 Location/Qualifiers

## FEATURES

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/organism="Beta vulgaris"
/mol_type="mRNA"
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-115"
/clone_type="storage root"
/lab_host="EMDHI08"
/clone_lib="WPIZ-ADIS-024-storage root"
/notes="Vector: PCWMSPORT6; Site 1: Sali, Site 2: Noct;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-Noct, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-Spline-cDNA-polyA-CC-Noct-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5396 AAAAAAAAAAAGAAAAATGAAAAAT 5425
Db 31 AAAAAAAAAAAGAAAAATGAAAAAT 2

RESULT 38
LOCUS A2597046 31 bp DNA linear GSS 13-DEC-2000
DEFINITION M06410K08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0410K08 R, genomic survey sequence.
ACCESSION A2597046.1 GI:11719236
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunng@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0410K08"
/sex="Male"
/lab_host="R. Coit strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```

```

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI:4732114|J9|AF12072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.4%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAAAAT 5422
Db 2 AAAAAAAAAAAGAAAAATGAAAAAT 31

RESULT 39
LOCUS H68053/c 28 bp mRNA linear EST 18-OCT-1995
DEFINITION Y74f04.r1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
IMAGE:211039 5' similar to gb:04970 CARBOXYPEPTIDASE M PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION H68053.1 GI:1026793
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 28)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.P., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Faveillo,A., Gish,W.,
Hawkins,M., Hiltman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,R., Moore,B., Morris,M., Parsons,J., Prange,C., Rickin,L.,
Roehlfing,T., Scheinberg,K., Soares,M.B., Tan,F., Thierry-Mieg,D.,
Trevaaskis,B., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 653
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 653 Std Error: 0.00
Seq primer: M13Rp1
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:378380"

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/db_xref="taxon:9606"
/clone="IMAGR:211039"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pTV73D (pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' , AACTGGAGAATTAATTAAAGATCTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTV73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fátima Bernaldo."

```

Query Match            0.4%; Score 21.6; DB 1; Length 28;  
Best Local Similarity   85.7%; Pred. No. 78;  
Matches   24; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

OY            3589 CATGTTCACGCGTCAATCTCAAATCC 3516  
DB            |||||  
28 CATGTTCACGCGTCAATCTCAAATCC 1

RESULT	40
LOCUS	AZ825156 29 bp DNA linear GSS 20-FEB-2001
DEFINITION	2M0100N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0100N08 F, genomic sequence.
ACCESSION	AZ825156
VERSION	AZ825156.1 GI:12995064
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 29) Dunn, P., Aovaggi, A., Barber, M., Baecorn, T., Duval, B., Hamil, C., Reilam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niedelhausern, A., Rose, M., Rose, R., Stokes, R., Tirney, A., von Richter, M., Rose, M., Rose, R., and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
TITLE	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0100 row: N column: 08 Seq primer: CGTTGTAACGACGCAGCAT Class: plasmid ends High quality sequence stop: 29.
JOURNAL	Location/Qualifiers
COMMENT	1..29 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0100N08" /sex="Male" /lab_host="B. Coli strain XL10-Gold, TI-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a
FEATURES	
SOURCE	

0.005 inch offset at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473114]pb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

RESULT 41
LOCUS AU267300
DEFINITION AU267300 VS Dictyostelium discoideum cDNA clone VSH345 5', mRNA
sequence.
ACCESSION AU267300
VERSION AU267300.1
KEYWORDS GI:20526098
SOURCE EST.
ORGANISM Dictyostelium discoideum
REFERENCE Dictyostelium discoideum
AUTHORS Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
1 (bases 1 to 30)
Matsuda,H., Morio,T., Salto,T., Kohara,Y., Koriki,E., Ochiai,H.,
Maeda,M., Williams,J.G., Takuchi,I. and Tanaka,Y.
Analyses of cDNAs from growth and slug stages of Dictyostelium
discoideum
Nucleic Acids Res. 32 (5), 1647-1653 (2004)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES
Source
location/Qualifiers
1..30
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:4689"
/clone="VSH345"
/bex="mat A"
/dev_stage="vegetative"
/clone_1b="VS"
Query Match 0.4%; Score 21.6; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 84;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5397 A A A T C A A A A A A A A A A A T C A A A A A T A A A 5425
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 A A A A A A A A A A A A A A A A A A A A A A A A A A 29
RESULT 42
LOCUS AZ443322
DEFINITION AZ443322 30 bp DNA linear GSS 04-OCT-2000
clone U06C1M0237L20 R, genomic survey sequence.

```

ACCESSION AZ443322  
 VERSION AZ443322.1 GI:10591190  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 30)  
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Haml, C., Islam, H., Longacre, S., Mahmood, M., Meenan, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0237 row: 1 column: 20  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 30.  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0237L20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21.6; DB 1; Length 30;  
 Best Local Similarity 85.7%; Pred. No. 84;  
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAAAGAAAAATGAAA 5420  
 |||||  
 Db 3 AAAAAAAAAAAGAAAAATGAAA 30  
 |||||  
 RESULT 43  
 LOCUS CF279536/c 29 bp mRNA linear EST 14-ANG-2003  
 DEFINITION 14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-N22, mRNA sequence.

ACCESSION CF279536  
 VERSION CF279536.1 GI:33656922  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 29)  
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 320 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 FEATURES  
 source  
 1.29  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="14ETL--05-N22"  
 /issue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1ib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
 |||||  
 Db 29 AAAAAAAAAAAGAAAAATGAAA 1  
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 RESULT 44  
 LOCUS CF299920 29 bp mRNA linear EST 15-ANG-2003  
 DEFINITION 7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C02, mRNA sequence.  
 ACCESSION CF299920  
 VERSION CF299920.1 GI:33671681  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 29)  
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 320 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 FEATURES  
 source  
 1.29

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-C02"
/cisue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAATTCAGAAAAAGAAAAATGAAA 5421  
 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 45  
 CFJ12601 29 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--08-G22, mRNA sequence.

ACCESSION CFJ12601 GI:33684362  
 VERSION CFJ12601.1 GI:33684362  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)  
 Kim,J.S., Jun,K.M., Cheong,P.U., Kim,M.U., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@jbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source location/Qualifiers  
 1..29  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--08-G22"  
 /cisue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAATTCAGAAAAAGAAAAATGAAA 5421  
 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 46  
 CN545237/c 29 bp mRNA linear EST 30-APR-2004  
 LOCUS EST 17181 Green Grape Skin Triplex2 library Vitis vinifera cDNA  
 DEFINITION clone B3CS00G1004G11 3', mRNA sequence.

ACCESSION CN545237  
 VERSION CN545237.1 GI:46909862  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)  
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,  
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,  
 Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
 or seeds) at Various Developmental Stages  
 Unpublished (2002)

JOURNAL CONTACT: Hamdi S.  
 UMR 619 - Equipe Biologie de la Vigne  
 Universite de Bordeaux I, Institut National de la Recherche  
 Agronomique  
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
 France  
 Tel: 00-33-(0)5-57-12-25-50  
 Fax: 00-33-(0)5-57-12-25-48  
 Email: s.hamdi@bordeaux.inra.fr  
 Seq primer: 17.

FEATURES  
 source location/Qualifiers  
 1..29  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3CS00G1004G11"  
 /dev\_stage="green stage"  
 /clone\_lib="Green Grape Skin Triplex2 library"  
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
 SfilA; Site\_2: SfilB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAATTCAGAAAAAGAAAAATGAAA 5421  
 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 47  
 CN546188/c 29 bp mRNA linear EST 30-APR-2004  
 LOCUS EST 18140 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA  
 DEFINITION clone B3CS00R1009D04 3', mRNA sequence.

ACCESSION CN546188  
 VERSION CN546188.1 GI:46910813  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)  
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,  
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,  
 Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
 or seeds) at Various Developmental Stages  
 Unpublished (2002)

## COMMENT

Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Université de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33- (0)5-57-12-25-50  
Fax: 00-33- (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## FEATURES

source

Location/Qualifiers

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1..29
/organism="Vitis vinifera"
/mol_type="rRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS08RL009D04"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"
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Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAATGAAA 5421

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 48

CNS46382/c

LOCUS 29 bp mRNA linear EST 30-APR-2004  
DEFINITION EST 18335 Green Grape Berry Lambda Triplex2 Library Vitis vinifera  
CDNA clone B3CS1XGB016D07 3', mRNA sequence.  
CNS46382  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Vitis vinifera

EST 46911007

Location/Qualifiers  
1..29  
/organism="Vitis vinifera"

/mol\_type="rRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS1XGB016D07"  
/dev\_stage="ripening stage"  
/clone\_1lb="Ripe Grape Skin Triplex2 Library"  
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

## REFERENCE

AUTHORS

Abbel, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Texier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)

## TITLE

JOURNAL

COMMENT

Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Université de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33- (0)5-57-12-25-50  
Fax: 00-33- (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## FEATURES

source

Location/Qualifiers

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/cultivar="Cabernet Sauvignon"
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/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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## Query Match

0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAATGAAA 5421

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 49

CNS46438/c

LOCUS 29 bp mRNA linear EST 30-APR-2004  
DEFINITION EST 18582 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
CDNA clone B3CS57RB007A03 3', mRNA sequence.  
CNS46438  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Vitis vinifera

EST 46911063

Location/Qualifiers  
1..29  
/organism="Vitis vinifera"

/mol\_type="rRNA"  
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/db\_xref="taxon:29760"  
/clone="B3CS57RB007A03"  
/dev\_stage="ripening stage"  
/clone\_1lb="Ripe Grape Berry Lambda Triplex2 Library"  
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

## REFERENCE

AUTHORS

Abbel, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Texier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)

## TITLE

JOURNAL

COMMENT

Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Université de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33- (0)5-57-12-25-50  
Fax: 00-33- (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## FEATURES

source

Location/Qualifiers

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/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007A03"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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Query Match 0.4%; Score 21; DB 1; Length 29;

Best Local Similarity 82.8%; Pred. No. 96;

Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAATGAAA 5421

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 50

CNS46557/c

LOCUS 29 bp mRNA linear EST 30-APR-2004  
DEFINITION EST 18701 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
CDNA clone B3CS58RB008C10 3', mRNA sequence.  
CNS46557  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Vitis vinifera

EST 46911182

Location/Qualifiers  
1..29  
/organism="Vitis vinifera"

/mol\_type="rRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS58RB008C10"  
/dev\_stage="ripening stage"  
/clone\_1lb="Ripe Grape Berry Lambda Triplex2 Library"  
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

REFERENCE	1 (bases 1 to 29)
AUTHORS	Abbal, P., Agrasse, A., Ageorges, A., Aranasova, R., Barrieu, F., Couture, C., Dedaïdechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Komtse, C. and Terrier, N.
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
FEATURES	Location/Qualifiers
source	1..29 /organism="Vitis vinifera" /mol_type="mRNA" /cultiivar="Cabernet Sauvignon" /db_xref="taxon:29740" /clone="B3CS58RB008C10" /dev_stage="ripe stage" /clone_1ib="Ripe Grape Berry Lambda Triplex2 Library" /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match	0.4%; Score 21; DB 1; Length 29;
Best Local Similarity	82.8%; Pred. No. 96;
Matches	24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	5393 AAAAAAAAAAGAAAAATGAAAA 5421       29 AAAAAAAAAAAAAAAAAAAAAA 1
Db	
RESULT 51	
LOCUS	AZ389566
DEFINITION	1M0150D21P Mouse 10kb plasmid UGCM1 library Mus musculus genomic clone UGCM10150D21 F, genomic survey sequence.
ACCESSION	AZ389566
VERSION	AZ389566.1 GI:10503274
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 29) Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamdi, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T., Rellay, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weis University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0..00 Plate: 0150 row: D column: 21 Seq primer: CGTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers 1..29
FEATURES	
source	1..29

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATACAAAAAGAAAAATGAAA 5421  
||||| ||||| ||||| ||||| |||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 52  
A2414283/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
SOURCE

A2414283 29 bp DNA linear GSS 03-OCT-2000  
M0186G12R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0186G12 R, genomic survey sequence.  
A2414283  
A2414283.1 GI:10538296  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellay, M., Rose, M., Rose, R., Stokes, R., Tingley, A., von  
Niederhausen, A. and Wright D. Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0188 row: G column: 12  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
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/organism="Mus musculus"  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0150D21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/cnote.lib="Mouse 10kb plasmid UGCGIM library"  
/cnote."Vector: PMD42nv: Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0251B05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5421  
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 53  
 AZ451930/c 29 bp DNA linear GSS 04-OCT-2000  
 LOCUS 1M0251B05R Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 DEFINITION clone UGGCM0251B05 R, genomic survey sequence.

ACCESSION AZ451930  
 VERSION AZ451930.1 GI:10608203  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0251 row: B column: 05  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0251B05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5421  
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 54  
 AZ468402/c 29 bp DNA linear GSS 04-OCT-2000  
 LOCUS 1M0281G24F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 DEFINITION clone UGGCM0281G24 F, genomic survey sequence.

ACCESSION AZ468402  
 VERSION AZ468402.1 GI:10626527  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0281 row: G column: 24  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 29.  
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 /mol\_type="genomic DNA"  
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 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
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Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAATGAAA 5421  
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 55  
 AZ486793/c 29 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0315N21 F, genomic survey sequence.  
 ACCESSION AZ486793  
 VERSION AZ486793.1 GI:10653915  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES  
 source  
 1. .29  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"

/clone="UUGC1M0315N21"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
 Best Local Similarity 82.8%; Pred. No. 96;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAATGAAA 5421  
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 56  
 AZ661709/c 29 bp DNA linear GSS 14-DEC-2000  
 LOCUS 1M0540K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0540K20 F, genomic survey sequence.  
 ACCESSION AZ661709  
 VERSION AZ661709.1 GI:11798855  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES  
 source  
 1. .29  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"



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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAATGAAA 5421  
|||||  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 57  
LOCUS AZ784208 29 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0026113R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCG2M0026113 R, genomic survey sequence.  
ACCESSION AZ784208  
VERSION AZ784208.1 GI:12919703  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0026 row: 1 column: 13  
Seq primer: CACACAGAAACAGCTATGACC  
Classes: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
1..29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0026113"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAATGAAA 5421  
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 58  
LOCUS AZ806470 29 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0068102R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
clone UGCG2M0068102 R, genomic survey sequence.  
ACCESSION AZ806470  
VERSION AZ806470.1 GI:12969849  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0068 row: 1 column: 02  
Seq primer: CACACAGAAACAGCTATGACC  
Classes: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
1..29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0068102"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAATGCAAAAAAGAAAAATGAAA 5421  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 59  
LOCUS AZ812242 29 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0078J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0078J15 R, genomic survey sequence.

ACCESSION AZ812242  
VERSION AZ812242.1 GI:12981296  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0078 row: J column: 15  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

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source location/Qualifiers

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/organism="Mus musculus"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAATGCAAAAAAGAAAAATGAAA 5421  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 60  
LOCUS AZ868731 29 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0180J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0180J02 R, genomic survey sequence.

ACCESSION AZ868731  
VERSION AZ868731.1 GI:13072338  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 29)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0180 row: L column: 02  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

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source location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0180J02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|9b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 61  
LOCUS TA334G090 29 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 334g09, reverse sequence,  
genomic survey sequence.  
ACCESSION AL491938 GI:11868238  
VERSION AL491938.1  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Alkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., Bl-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
SUBMITTED (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).

DETAILS OF T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source  
1. 29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:5691"  
/clone="334g09"

Query Match 0.4%; Score 21; DB 1; Length 29;  
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Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 62  
LOCUS AG193759 29 bp DNA linear GSS 06-MAR-2004  
DEFINITION Pan troglodytes DNA, clone: RP43-071B06.T7, genomic survey  
sequence.  
ACCESSION AG193759  
VERSION AG193759.1 GI:45225935  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

## REFERENCE

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of library RP-43

## JOURNAL

2 (bases 1 to 29)  
Unpublished  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
DIRECT SUBMISSION  
SUBMITTED (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC),  
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea  
(E-mail: redstone@mail.kribb.re.kr, URL: <http://pms.grc.kribb.re.kr/>,  
Tel: 82-42-866-7101, Fax: 82-42-860-4409)  
Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the Red process and may have higher chance  
of clone tracking errors.

## COMMENT

PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBAC3.6  
R Site 1 : EcoRI.  
R Site 2 : EcoRI.  
Location/Qualifiers  
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/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-071B06.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_11b="RP-43 Chimpanzee Male BAC library"

## FEATURES

source  
1. 29  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-071B06.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_11b="RP-43 Chimpanzee Male BAC library"

Query Match 0.4%; Score 21; DB 1; Length 29;  
Best Local Similarity 82.8%; Pred. No. 96;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 63  
LOCUS AL038650 30 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566I1846\_r1.566 (synonym: hnfcd2) Homo sapiens cDNA clone  
AL038650  
ACCESSION AL038650  
VERSION AL038650.1 GI:49682176  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 30)  
Ottewill, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and

TITLE  
JOURNAL  
COMMENT  
Wiemann,S.  
EST (Otcenwaeider, et al.)  
Unpublished (1999)  
Contact: MIPS

FEATURES  
source  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.  
Location/Qualifiers  
1..30

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="DKFZp5611846"  
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/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone.lib="566 (synonym: hfxd2)"  
/note="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

Query Match 0.4%; Score 21; DB 1; Length 30;  
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Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 64  
LOCUS BG666435 30 bp mRNA linear EST 30-APR-2001  
DEFINITION DRACRC02 Rat DRG Library Rattus norvegicus cDNA clone DRACRC02 5',  
mRNA sequence.  
ACCESSION BG666435  
VERSION BG666435.1 GI:13888357  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,  
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.  
Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
JOURNAL MEDLINE  
PUBMED 22056133  
12060780  
CONTACT: Zhang Xu  
Laboratory of Sensory System  
Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China  
Tel: 86-21-64748700-121  
Fax: 86-21-64713446  
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)  
PCR Primers  
FORWARD: T3  
BACKWARD: T7  
Seq primer: T3  
POLYA=No.

FEATURES  
source  
Location/Qualifiers  
1..30

/organism="Rattus norvegicus"  
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/db\_xref="taxon:10116"  
/clone="DRACRC02"  
/sex="male"

/tissue\_type="dorsal root ganglion"  
/dev\_stage="adult"  
/clone.lib="Rat DRG Library"  
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Best Local Similarity 82.8%; Pred. No. 99;  
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QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 65  
LOCUS BG665511 30 bp mRNA linear EST 29-MAY-2001  
DEFINITION 602783643r1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4909811 5',  
mRNA sequence.  
ACCESSION BG665511  
VERSION BG665511.1 GI:14216051  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eumaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strusberg, Ph.D.  
Email: c9apbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL0809 row: e column: 12  
High quality sequence stop: 30.

FEATURES  
source  
Location/Qualifiers  
1..30

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4909811"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone.lib="NCI\_CGAP\_SG2"  
/note="Organ: Salivary gland; Vector: pCMV-SPORT6; Site\_1:  
NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo  
dT. Average insert size 1.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 66  
LOCUS CP280699/c 30 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14FTL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14FTL),  
Oryza sativa (japonica cultivar-group) cDNA clone 14FTL--07-H15,  
mRNA sequence.  
ACCESSION CP280699  
VERSION CP280699.1 GI:33658085  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

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ORGANISM      Oryza sativa (japonica cultivar-group)
LOCUS         CF292086
DEFINITION   14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
              sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
              sequence.
ACCESSION    CF292086
VERSION      CF292086.1
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 30)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /db_xref="taxon:39947"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /dev_stage="14 days after germination"
      /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."
  
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Query Match      0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Ory 5393 AAAAAATACAAAAAGAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 68
CF299555/c
LOCUS         CF299555
DEFINITION   7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K01, mRNA
              sequence.
ACCESSION    CF299555
VERSION      CF299555.1
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 30)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
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              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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    1..30
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      /issue_type="leaf"
      /dev_stage="7 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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      RT-PCR."
  
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ABF--08-C19, mRNA sequence.  
 ACCESSION CF312417  
 VERSION CF312417.1 GI:33684178  
 KEYWORDS EST.  
 SOURCE Oriza sativa (japonica cultivar-group)  
 ORGANISM Oriza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 30)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--08-C19"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABP)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 21; DB 1; Length 30;  
 Best Local Similarity 82.8%; Pred. No. 99;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAATGCAAAAAAGAAAAATGAAA 5421  
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 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

Db  
 |||||  
 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 70  
 CF322226 30 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD--13-M02.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--13-M02, mRNA sequence.  
 ACCESSION CF322226  
 VERSION CF322226  
 KEYWORDS EST.  
 SOURCE Oriza sativa (japonica cultivar-group)  
 ORGANISM Oriza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 30)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.  
 FEATURES  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HD--13-M02"  
 /tissue\_type="callus"  
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 /lab\_host="E.coli DH10B"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA (20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 21; DB 1; Length 30;  
 Best Local Similarity 82.8%; Pred. No. 99;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAATGCAAAAAAGAAAAATGAAA 5421  
 |||||  
 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

Db  
 |||||  
 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 71  
 CF327835 30 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--02-H17, mRNA  
 sequence.  
 ACCESSION CF327835  
 VERSION CF327835  
 KEYWORDS EST.  
 SOURCE Oriza sativa (japonica cultivar-group)  
 ORGANISM Oriza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 30)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
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 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /clone="NACL--02-H17"  
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 /dev\_stage="proliferated callus on 2M6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 30;  
 Best Local Similarity 82.8%; Pred. No. 99;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	5393	AAAAAAAAATCAAAAAAAAAAGAAAAATGAAAA	5421
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	29
RESULT 72			
LOCUS	CF336555/c		
DEFINITION	CF336555	30 bp	mRNA linear EST 18-AUG-2003
	UPT--06-K13.g1	AluUPT-overexpressing transgenic rice plasmid cDNA library (UPT)	Oryza sativa (japonica cultivar-group) cDNA clone
	UPT--06-K13,	mRNA sequence.	
ACCESSION	CF336555		
VERSION	CF336555.1	GI:33821487	
KEYWORDS	EST		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzaceae; Oryza.		
REFERENCE	1	(bases 1 to 30)	
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.		
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	/mol_type="mRNA"		
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	/dev_stage="14 days after germination"		
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	/clone_idb="AcUPT-overexpressing transgenic rice plasmid cDNA library (UPT)"		
	/note="Vector: pCR4-TOPO, Site_1: EcoRI, Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."		
Query Match	0.4%	Score 21;	DB 1;
Beat Local Similarity	82.8%	Pred. No. 99;	
Matches	24;	Conservative 0;	Mismatches 5;
		Indels 0;	Gaps 0;
QY	5393	AAAAAAAAATCAAAAAAAAAAGAAAAATGAAAA	5421
Db	30	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	2
RESULT 73			
LOCUS	CNS45845/c		
DEFINITION	CNS45845	30 bp	mRNA linear EST 30-APR-2004
	EST 17789	Ripe Grape Skin T1p1ex2 Library	Vitis vinifera cDNA
ACCESSION	CNS45845		
VERSION	CNS45845.1	GI:46910470	
KEYWORDS	EST		
SOURCE	Vitis vinifera		
ORGANISM	Vitis vinifera		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.		
	1 (bases 1 to 30)		
REFERENCE	Abdel,P., Agashe,A., Ageorges,A., Atanasova,R., Barreau,F., Couture,C., Dedaldechamp,F., Delrot,S., Gillesant,D., Grimplet,J.,		

```

TITLE
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
JOURNAL
Contact: Hamdi S.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
COMMENT
Seq primer: T7.
FEATURES
SOURCE
Location/Qualifiers
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/dev_stage="ripening stage"
/clone_1db="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: lambda Triplex2; Site_1:
SF1A, Site_2: SF1B, Oriented library"
OR
5393 AAAAAATACAAAAGAAAGAAGAAA 5421
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Gaps 0;
OCY 5393 AAAAAATACAAAAGAAAGAAGAAA 5421
||||| ||||| ||||| |||||
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 74
CN545913/c
LOCUS CN545913 30 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17857 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION clone B3CS00RL006C10 3', mRNA sequence.
VERSION CN545913
KEYWORDS CN545913.1 GI:46910538
EST.
Vitis vinifera
Vitis vinifera
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Cubal,P., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
CONTACT: Hamdi S.
JOURNAL
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
COMMENT
Seq primer: T7.
FEATURES
SOURCE
Location/Qualifiers
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/organism="Vitis vinifera"
/mol_type="mRNA"
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/clone.lib="Ripe Grape Skin Triplex2 Library"  
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SflIA; Site\_2: SflIB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 75  
CN546459/c 30 bp mRNA linear EST 30-APR-2004  
LOCUS CN546459/c  
DEFINITION EST 18603 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
ACCESSION CN546459  
VERSION CN546459.1 GI:46911084  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera

REFERENCE  
AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romeu, C. and Terrier, N.  
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

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Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 76  
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LOCUS CN546474/c  
DEFINITION EST 18618 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
ACCESSION CN546474  
VERSION CN546474.1 GI:46911099  
KEYWORDS EST.  
SOURCE Vitis vinifera

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/culturvar="Cabernet Sauvignon"  
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/clone="B3CS57RB007C01"  
/dev\_stage="ripe stage"  
/clone.lib="Ripe Grape Berry Lambda Triplex2 Library"  
/note="Organ: Fruit without seeds; Vector: Lambda  
Triplex2; Site\_1: SflIA; Site\_2: SflIB; Oriented library"

## ORGANISM

Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.

## REFERENCE

1 (bases 1 to 30)  
Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romeu, C. and Terrier, N.  
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hamdi S.  
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
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Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## JOURNAL

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Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## FEATURES

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Triplex2; Site\_1: SflIA; Site\_2: SflIB; Oriented library"

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Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 77  
CN546789/c 30 bp mRNA linear EST 30-APR-2004  
LOCUS CN546789/c  
DEFINITION EST 18560 Turning Grape Berry Lambda Triplex2 Library Vitis  
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ACCESSION CN546789  
VERSION CN546789.1 GI:46915099  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 30)  
Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romeu, C. and Terrier, N.  
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
JOURNAL Unpublished (2002)  
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Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

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Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romeu, C. and Terrier, N.  
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
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JOURNAL Unpublished (2002)  
COMMENT Contact: Hamdi S.  
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Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

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Tel: 00-33-(0)5-57-12-25-50  
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Email: s.hamdi@bordeaux.inra.fr  
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Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

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Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

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France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

Unpublished (2002)  
Contact: Hamdi S.  
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Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

Unpublished (2002)  
Contact: Hamdi S.  
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Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.



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/organism="Vitis vinifera"
/mol_type="rRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS18T08G04"
/dev stage="yeastson stage"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAATGAAA 5421
DB 30 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 78
LOCUS AZ357603 30 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0099H17F Mouse 10kb plasmid UGCM1 library Mus musculus genomic
clone UGCM0099H17 F, genomic survey sequence.
ACCESSION AZ357603
VERSION AZ357603.1 GI:10471303
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: H column: 17
Seq primer: CGTTGTAACACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0099H17"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-."
/clone_lib="Mouse 10kb plasmid UGCM1 library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

```

10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAATGAAA 5421
DB 30 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 79
LOCUS AZ455741 30 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0258D16F Mouse 10kb plasmid UGCM1 library Mus musculus genomic
clone UGCM0258D16 F, genomic survey sequence.
ACCESSION AZ455741
VERSION AZ455741.1 GI:10613866
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: D column: 16
Seq primer: CGTTGTAACACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0258D16"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-."
/clone_lib="Mouse 10kb plasmid UGCM1 library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 80  
A2481739/c 30 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0306N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0306N12 F, genomic survey sequence.

ACCESSION A2481739  
VERSION A2481739.1 GI:10642804  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathli; Muridae; Murinae; Mus. 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0306 Row: N Column: 12  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

FEATURES  
Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0306N12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 81  
A2582114/c 30 bp DNA linear GSS 13-DEC-2000  
LOCUS A2582114/c  
DEFINITION 1M0374U17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0374U17 F, genomic survey sequence.

ACCESSION A2582114  
VERSION A2582114.1 GI:11700674  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathli; Muridae; Murinae; Mus. 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0374 Row: J Column: 17  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 30.

FEATURES  
Location/Qualifiers

source

1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0374U17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 82  
AG191161/c 30 bp DNA linear GSS 06-MAR-2004  
LOCUS AG191161  
DEFINITION Pan troglodytes DNA, clone: RP43-066P20.T7, genomic survey  
sequence.  
ACCESSION AG191161 GI:45223337  
VERSION AG191161.1  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1  
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
TITLE BAC end sequences of library RP-43  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 30)  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Direct Submission  
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);  
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea  
(E-mail: redstone@mail.krribb.re.kr, URL: http://pns.grc.krribb.re.kr/,  
Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : PBACg3.6  
R.Site 1 : EcorI  
R.Site 2 : EcorI.  
Location/Qualifiers  
1. 30  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-066P20.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES  
source

Query Match 0.4%; Score 21; DB 1; Length 30;  
Best Local Similarity 82.8%; Pred. No. 99;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421  
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 83  
AU267990/c 29 bp mRNA linear EST 26-APR-2004  
LOCUS AU267990

DEFINITION AU267990 VS Dictyostelium discoideum cDNA clone VSH801 5', mRNA  
sequence.

ACCESSION AU267990  
VERSION AU267990.1 GI:20526788  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, E., Ochiai, H.,  
Maeda, M., Williams, J.G., Takeuchi, I. and Tanaka, Y.  
TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium  
discoideum  
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hidekobio@tsukuba.ac.jp.

FEATURES  
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/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH801"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VGS"

Query Match 0.4%; Score 20.8; DB 1; Length 29;  
Best Local Similarity 91.7%; Pred. No. 1e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5391 TTTAAAAATACAAAAAGAAAA 5414  
Db 29 TTTAAAAATACAAAAAGAAAA 6

RESULT 84  
AZ941721/c 27 bp DNA linear GSS 26-APR-2001  
LOCUS AZ941721  
DEFINITION 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0201004 R, genomic survey sequence.  
ACCESSION AZ941721  
VERSION AZ941721.1 GI:13804440  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00  
Plate: 0201 row: O column: 04  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends

FEATURES  
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High quality sequence stop: 27.  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0201004"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 27;  
Best Local Similarity 85.2%; Pred. No. 99;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5394 AAAAAATACAAAGAAAAATGAA 5420  
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Db 27 AAAAAAAAAAAAAAAAAAGAA 1

RESULT 85  
A2970621/c 27 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0243N14R Mouse 10kb plasmid UUCG2M library Mus musculus genomic  
DEFINITION clone UUCG2M0243N14 R, genomic survey sequence.  
ACCESSION A2970621 GI:13841848  
VERSION A2970621.1 GI:13841848  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Haml,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0243 row: N column: 14  
Seq primer: CACACAGGAACGCTATGAC  
Classes: plasmid ends  
High quality sequence stop: 27.

FEATURES  
source  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0243N14"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 27;  
Best Local Similarity 85.2%; Pred. No. 99;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAGAAAAATGAA 5419  
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Db 27 AAAAAAAAAAAAAAAAAAGAA 1

RESULT 86  
CF307749/c 28 bp mRNA linear BST 15-AUG-2003  
LOCUS ABF--01-E17.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone ABF--01-E17, mRNA sequence.  
ACCESSION CF307749  
VERSION CF307749.1 GI:33679510  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eupharbioidae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongui University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..28  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF--01-E17"  
/issue\_type="leaf"

/dev stage="14 days after germination"  
 /lab host="R.coli DH10B"  
 /clone lib="ABP3-overexpressing transgenic rice plasmid  
 cDNA library (ABP)"  
 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 20.6; DB 1; Length 28;  
 Best Local Similarity 85.2%; Pred. No. 1e+02;  
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAAAAATGAAAA 5421  
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 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 87  
 AZ824574/c 28 bp DNA linear GSS 20-FRB-2001  
 LOCUS  
 DEFINITION 2M0099D17P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0099D17 F, genomic survey sequence.  
 ACCESSION AZ824574  
 VERSION AZ824574.1 GI:12994482  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0099 row: D column: 17  
 Seq primer: CCGTGTAAACAGCGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0099D17"  
 /sex="Male"  
 /lab host="R. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel

electroporesis. Vector DNA was prepared from a derivative  
 of PMD42 (gi4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 28;  
 Best Local Similarity 85.2%; Pred. No. 1e+02;  
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAAAAATGAAAA 5421  
 |||||  
 Db 28 AAAAAATACAAAAAGAAAAATGAAAA 2

RESULT 88  
 AZ836072/c 28 bp DNA linear GSS 20-FRB-2001  
 LOCUS  
 DEFINITION 2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0130K08 R, genomic survey sequence.  
 ACCESSION AZ836072  
 VERSION AZ836072.1 GI:13005980  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0130 row: K column: 08  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0130K08"  
 /sex="Male"  
 /lab host="R. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel

electroporesis. Vector DNA was prepared from a derivative  
 of PMD42 (gi4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

of pWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 28;  
Best Local Similarity 85.2%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5394 AAAAAAAAAAAGAAAAATGAA 5420  
Db 28 AAAAAAAAAAAGAAAAATGAA 2

RESULT 89  
BQ583967/c  
LOCUS  
DEFINITION S013297-024-004-B01-T7 MP12-ADIS-024-inflorescence Beta vulgaris  
ACCESSION BQ583967 29 bp mRNA linear EST 06-DEC-2002  
VERSION S013297-024-004-B01 3-PRIME, mRNA sequence.  
KEYWORDS  
SOURCE BQ583967.1 GI:26113544  
ORGANISM Beta vulgaris

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS  
1 (bases 1 to 29)  
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,  
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radloff, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mp12-koeln.mpg.de  
Insert Length: 29 Std Error: 0.00  
Places: 4 row: B column: 01  
Seq primer: T7; GTAATACGACTCTACTATAGGCG.  
Location/Qualifiers

FEATURES  
source

1..29  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:182728"  
/db\_xref="taxon:161934"  
/clone="024-004-B01"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_11b="MP12-ADIS-024-inflorescence"  
/note="Vector: PCWVSPT06; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 20.6; DB 1; Length 29;  
Best Local Similarity 85.2%; Pred. No. 1.1e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 5393 AAAAAAAAAAAGAAAAATGAA 5419  
Db 27 AAAAAAAAAAAGAAAAATGAA 1

RESULT 90  
CF317007/c  
LOCUS  
DEFINITION HD--06-114.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--06-114, mRNA sequence.  
ACCESSION CF317007 25 bp mRNA linear EST 15-AUG-2003  
VERSION CF317007  
KEYWORDS  
SOURCE CF317007.1 GI:33688768  
ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
1 (bases 1 to 25)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1..25  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HD--06-114"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_11b="OsHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice histone Deacetylase overexpression  
line."

Query Match 0.4%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAAAGAAAAA 5415  
Db 25 TTTAAAAAATACAAAAAAGAAAAA 1

RESULT 91  
AL038686  
LOCUS  
DEFINITION DKFZP566J0546\_r1 566 (synonym: hfkx2) Homo sapiens cDNA clone  
DKFZP566J0546, mRNA sequence.  
ACCESSION AL038686 26 bp mRNA linear EST 06-JUL-2004  
VERSION AL038686  
KEYWORDS  
SOURCE DKFZP566J0546.1 GI:49682186  
ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 26)

AUTHORS Ootenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 TITLE EST (Ootenwaelder, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS

FEATURES Ingoltseder Landstr.1, D-85764 Neuherberg, Germany.  
 Location/Qualifiers

## source

1.26  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZ566J0546"  
 /tissue\_type="kidney"  
 /dev\_stage="fetal"  
 /lab\_host="X1-2Blue"  
 /clone\_1ib="566 (synonym: hfkd2)"  
 /note="Vector: PAMPI; Site\_1: NotI; Site\_2: SalI"

Query Match 0.4%; Score 20.2; DB 1; Length 26;  
 Best Local Similarity 88.0%; Pred. No. 1.1e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAAGAAAAA 5415  
 Db 1 TTTAAAAAATACAAAAAGAAAAA 25

RESULT 92 26 bp mRNA linear EST 15-AUG-2003  
 CF299646/c 7LEAF--03-L24, b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 LOCUS sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L24, mRNA  
 DEFINITION sequence.

ACCESSION CF299646 GI:33671407  
 VERSION CF299646  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.T., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 321 6355  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

## source

1.26  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--03-L24"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1ib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.4%; Score 20.2; DB 1; Length 26;  
 Best Local Similarity 88.0%; Pred. No. 1.1e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5390 ATTAAAAAATACAAAAAGAAAAA 5414  
 Db 25 ATTAAAAAATACAAAAAGAAAAA 1

RESULT 93 28 bp mRNA linear EST 18-AUG-2003  
 CF337400 JMT--07-N04, g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 LOCUS library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 DEFINITION JMT--07-N04, mRNA sequence.

ACCESSION CF337400 GI:33823200  
 VERSION CF337400  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 28)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.T., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 321 6355  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

## source

1.28  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="JMT--07-N04"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1ib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jaemolnate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.4%; Score 20.2; DB 1; Length 28;  
 Best Local Similarity 88.0%; Pred. No. 1.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAAGAAAAA 5415  
 Db 1 TTTAAAAAATACAAAAAGAAAAA 25

RESULT 94 28 bp mRNA linear EST 27-OCT-1999  
 A1971979 WV30h06, x1 NCI CGAP Ovis Homo sapiens cDNA clone IMAGE:2531099 3'  
 LOCUS similar to TR:063545 063545 NM\_001000000 SUBMIT 5; contains  
 DEFINITION TARI, b1 TARI repetitive element; mRNA sequence.

ACCESSION A1971979 GI:5768805  
 VERSION A1971979  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 28)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

**JOURNAL**  
**COMMENT**  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9abbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arranged by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

**FEATURES**  
 source  
 Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..28  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2531099"  
 /tissue\_type="fibrothecoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Ov18"  
 /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAGTGGAGCGCGCGACATTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Patricia Bonaldo. "

**Query Match**  
 Best Local Similarity 0.4%; Score 20; DB 1; Length 28;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy** 5386 AAGAAATTAATAATACAAAAAGAAAA 5413  
 Db 1 AAGAAAAAACCAACCAAAAGAAACA 28

**RESULT 95**  
 AJ666435/c 28 bp mRNA linear EST 28-JUN-2004  
**LOCUS** AJ666435 CSEQRAN09 Sus scrofa cDNA clone C0000033\_L21, mRNA  
**DEFINITION** AJ666435 CSEQRAN09 Sus scrofa cDNA clone C0000033\_L21, mRNA  
**ACCESSION** AJ666435  
**VERSION** AJ666435  
**KEYWORDS** EST.  
**SOURCE** Sus scrofa (pig)  
**ORGANISM** Sus scrofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
**REFERENCE** 1 (bases 1 to 28)  
**AUTHORS** Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
**TITLE** Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: BluescriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
 Location/Qualifiers

**source**  
 1..28  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0000033\_L21"  
 /tissue\_type="placenta"  
 /clone\_lib="CSEQRAN09"  
 /note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

**Query Match**  
 Best Local Similarity 0.4%; Score 20; DB 1; Length 28;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy** 5393 AAAAAATACAAAAAGAAAAATGAAA 5420  
 Db 28 AAAAAAATTAATAATAAAAAA 1

**RESULT 96**  
 AM332443/c 28 bp mRNA linear EST 31-JAN-2000  
**LOCUS** AM332443 S887 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
**DEFINITION** AM332443 S887 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
**ACCESSION** AM332443  
**VERSION** AM332443.1 GI:6828800  
**KEYWORDS** EST.  
**SOURCE** Pneumocystis carinii  
**ORGANISM** Pneumocystis carinii  
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae; Pneumocystis.  
**REFERENCE** 1 (bases 1 to 28)  
**AUTHORS** Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.  
**TITLE** Expressed sequence tags from Pneumocystis carinii  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staben@pop.uky.edu.  
 Location/Qualifiers  
 1..28  
 /organism="Pneumocystis carinii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4754"  
 /lab\_host="E. coli"  
 /clone\_lib="AGS-1"  
 /note="Vector: lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

**Query Match**  
 Best Local Similarity 0.4%; Score 20; DB 1; Length 28;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy** 5393 AAAAAATACAAAAAGAAAAATGAAA 5420  
 Db 28 AAAAAAATTAATAATAAAAAA 1

**RESULT 97**  
 CF282351/c 28 bp mRNA linear EST 14-AUG-2003  
**LOCUS** CF282351 14E7L--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14E7L)  
**DEFINITION** 14E7L--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14E7L)  
 Oryza sativa (Japanica cultivar-group) cDNA clone 14E7L--09-N05, mRNA sequence.



```

ACCESSION   CF282351
VERSION     CF282351.1
KEYWORDS    EST
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..28
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="14ETL--09-N05"
            /issue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice etiolated leaf plasmid cDNA library
            (14ETL)"
            /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAAATGAAA 5420
    |||||
    28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 98
CF321885      28 bp      mRNA      linear      EST 15-AUG-2003
HD-13-E16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-13-E16, mRNA sequence.

ACCESSION     CF321885
VERSION       CF321885.1
KEYWORDS      GI:33693646
SOURCE        EST.
ORGANISM      Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 28)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--06-U14"
            /issue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA (20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAAATGAAA 5420
    |||||
    28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 99
CF330748      28 bp      mRNA      linear      EST 18-AUG-2003
NACL--06-U14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-U14, mRNA
sequence.

ACCESSION     CF330748
VERSION       CF330748.1
KEYWORDS      GI:33809717
SOURCE        EST.
ORGANISM      Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 28)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--06-U14"
            /issue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

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```

RESULT 100
CF330938      28 bp      mRNA      linear      EST 18-ANG-2003
LOCUS        NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION   sativa (japonica cultivar-group) cDNA clone NACL--06-N19, mRNA
sequence.
ACCESSION   CF330938
VERSION     CF330938.1 GI:33810102
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
             Location/Qualifiers
             1..28
             /organism="Oryza sativa (japonica cultivar-group)"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:39347"
             /clone="NACL--06-N19"
             /tissue_type="callus"
             /dev_stage="proliferated callus on 2N6 media for 30 days"
             /lab_host="E.coli DH10B"
             /clone_1ib="Rice callus plasmid cDNA library (NACL)"
             /note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped
             with oligoribonucleotides and then used as templates for
             RT-PCR."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 101
CNS46364      28 bp      mRNA      linear      EST 30-APR-2004
LOCUS        EST 18317 Green Grape Berry Lambda Triplex2 library Vitis vinifera
DEFINITION   cDNA clone B3CS1XGB016C01 3', mRNA sequence.
ACCESSION   CNS46364
VERSION     CNS46364.1 GI:46910989
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
              1 (bases 1 to 28)
              /dev_stage="veraison stage"
              /clone_1ib="Turning Grape Berry Lambda Triplex2 library"
              /note="Organ: Fruit without seeds; Vector: Lambda
              Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

REFERENCE   1 (bases 1 to 28)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
             Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
             Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
             or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.

```

```

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..28
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007H02"
/dev_stage="veraison stage"
/clone_1ib="Turning Grape Berry Lambda Triplex2 library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
Db      28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 102
CNS46703      28 bp      mRNA      linear      EST 30-APR-2004
LOCUS        EST 18474 Turning Grape Berry Lambda Triplex2 library Vitis
DEFINITION   vinifera cDNA clone B3CS37TB007H02 3', mRNA sequence.
ACCESSION   CNS46703
VERSION     CNS46703.1 GI:46911328
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
              1 (bases 1 to 28)
              /dev_stage="veraison stage"
              /clone_1ib="Turning Grape Berry Lambda Triplex2 library"
              /note="Organ: Fruit without seeds; Vector: Lambda
              Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

REFERENCE   1 (bases 1 to 28)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
             Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
             Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
             or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
             UMR 619 - Equipe Biologie de la Vigne
             Universite de Bordeaux I, Institut National de la Recherche
             Agronomique
             71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
             France
             Tel: 00-33-(0)5-57-12-25-50
             Fax: 00-33-(0)5-57-12-25-48
             Email: s.hamdi@bordeaux.inra.fr
             Seq primer: T7.
             Location/Qualifiers
             1..28
             /organism="Vitis vinifera"
             /mol_type="mRNA"
             /cultivar="Cabernet Sauvignon"
             /db_xref="taxon:29760"
             /clone="B3CS37TB007H02"
             /dev_stage="veraison stage"
             /clone_1ib="Turning Grape Berry Lambda Triplex2 library"
             /note="Organ: Fruit without seeds; Vector: Lambda
             Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.4%; Score 20; DB 1; Length 28;

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Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAAATGAA 5420  
|||||  
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 103

AZ399637 28 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ399637.c  
DEFINITION 1M0165N04R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0165N04 R, genomic survey sequence.

ACCESSION AZ399637  
VERSION AZ399637.1 GI:10514711

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0165 row: N column: 04  
Seq primer: CACACAGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers

## FEATURES

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1..28  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0165N04"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD2nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;  
Best Local Similarity 82.1%; Pred. No. 1.2e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAAATGAA 5420  
|||||  
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 104

AZ401766 28 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ401766  
DEFINITION 1M0168008R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG1M0168008 R, genomic survey sequence.

ACCESSION AZ401766  
VERSION AZ401766.1 GI:10516840

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0168 row: O column: 08  
Seq primer: CACACAGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers

## FEATURES

source

1..28  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0168008"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD2nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;  
Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5420  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 105  
 AZ471744 28 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ471744/c  
 DEFINITION clone UGCLM0286K08 R, genomic survey sequence.

ACCESSION AZ471744  
 VERSION AZ471744.1 GI:10629965  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 28)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0286 row: K column: 08  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers

## FEATURES

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1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLM0286K08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCLM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;  
 Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5420  
 |||||  
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 106  
 AZ493138 28 bp DNA linear GSS 05-OCT-2000  
 LOCUS AZ493138  
 DEFINITION 1M0327F02R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0327F02 R, genomic survey sequence.

ACCESSION AZ493138  
 VERSION AZ493138.1 GI:10663359  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 28)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0327 row: F column: 02  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers

## FEATURES

source

1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLM0327F02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCLM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;  
 Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAAAGAAAAATGAAA 5420



```

RESULT 109
AZ824519/c
LOCUS      28 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M009109F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M009109 F, genomic survey sequence.
ACCESSION  AZ824519
VERSION     AZ824519.1  GI:12994427
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE      Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0099 row: 1 column: 09
            Seq primer: CGTTGTAAACGACGCCACGT
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES   Location/Qualifiers
            1..28
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M009109"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_1fb="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5420
    ||||| ||||| ||||| ||||| |||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 110
AZ833425
LOCUS      28 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0115D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0115D04 R, genomic survey sequence.
ACCESSION  AZ833425
VERSION     AZ833425.1  GI:13003333
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE      Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0115 row: D column: 04
            Seq primer: CACACGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES   Location/Qualifiers
            1..28
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0115D04"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_1fb="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5420
    ||||| ||||| ||||| ||||| |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

```

```

RESULT 111
AZ866569/c
LOCUS      28 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION 2M0177B08F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
            clone UGCG2M0177B08 F, genomic survey sequence.
ACCESSION  AZ866569
VERSION     AZ866569.1  GI:13068007
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 28)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
            Iselm,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
            Niederhausern,A. and Wright,D., Weiss,R.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL
COMMENT    Contract: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0177 row: B column: 08
            Seq primer: CGTTGTAACGACGCGCACT
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES
source
1..28
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UGCG2M0177B08"
    /sex="Male"
    /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_1fb="Mouse 10kb plasmid UGCG1M library"
    /note="Vector: PMD29v. Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (GI:4732114|db|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent R. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      5393 AAAAAATTCAGAAAAGAAAATGAAA 5420
DB      28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

TA291A01Q
LOCUS      28 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 291a01, reverse sequence,
            genomic survey sequence.
ACCESSION  AL486613
VERSION     AL486613.1  GI:11853602
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Trypanosoma brucei
REFERENCE  1 (bases 1 to 28)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
            Direct Submision
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
            Barrell, Oxford University Press, 1999).
            Email: nhl@sanger.ac.uk
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..28
    /organism="Trypanosoma brucei"
    /mol_type="genomic DNA"
    /strain="TRU927"
    /db_xref="taxon:5691"
    /clone="291a01"
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      5393 AAAAAATTCAGAAAAGAAAATGAAA 5420
DB      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

```

```

RESULT 113
TA29A09P/c
LOCUS      28 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 29a09, forward sequence,
            genomic survey sequence.
ACCESSION  AL453073
VERSION     AL453073.1  GI:11854584
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Trypanosoma brucei
REFERENCE  1 (bases 1 to 28)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
            Direct Submision
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared

```

to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1..28  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="29a09"

Query Match 0.4%; Score 20; DB 1; Length 28;  
Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5398 AATACAAAGAAAGAAATGAAATGAA 5425  
DB 28 AAAAAAAAAAAAAAAAAATAAAAAAAA 1

## RESULT 114

TA379D11P/c 28 bp DNA linear GSS 13-DEC-2000

DEFINITION T. brucei sheared genomic DNA clone 379d11, forward sequence,  
genomic survey sequence.

ACCESSION AL497637

VERSION AL497637.1 GI:11873359

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 28)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

Location/Qualifiers

1..28

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

/db\_xref="taxon:5691"

/clone="379d11"

## FEATURES

source

1..28  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="379d11"

Query Match 0.4%; Score 20; DB 1; Length 28;  
Best Local Similarity 82.1%; Pred. No. 1.2e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAGAAATGAAA 5420

||||| ||||| ||||| ||||| |||||

DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 115

BG929133/c 25 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC34-1-B8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

sequence.

ACCESSION BG929133

VERSION BG929133.1 GI:14323656

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 25)

Kumar, S., Connor, J.R., Dadds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Satche, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lark, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteochondritic cartilage cDNA libraries

Osteochondr. Cartil. 9 (7), 641-653 (2001)

21482651

11597177

JOURNAL PUBMED

COMMENT

Contact: Sanjay Kumar

UM2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: 17.

## FEATURES

source

1..25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_id="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
directional"

Query Match 0.4%; Score 19.8; DB 1; Length 25;  
Best Local Similarity 91.3%; Pred. No. 1.1e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAGAAAGAA 5415

DB 25 AAAAAAAAAACATTAAGAAAAA 3

## RESULT 116

CD028815 27 bp mRNA linear EST 07-MAY-2003

DEFINITION mgcse010xa10f.b Magnaporthe grisea CS uni-zag XR Library Magnaporthe

grisea cDNA clone mgcse010xa10 5', mRNA sequence.

ACCESSION CD028815

VERSION CD028815.1 GI:30410271

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 27)

Ebbole, D.O., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,

Bhatterai, K. and Dean, R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe

grisea

Unpublished (2002)

JOURNAL

COMMENT

Contact: Ebbole DU

Department of Plant Pathology & Microbiology



Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact person;  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgc010 row: A column: 10  
 Seq primer: T3.

## FEATURES

source

1. .27  
 /organism="Magnaporthe grisea"  
 /mol\_type="rRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgc010x10"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="conidia"  
 /clone\_1lb="Magnaporthe grisea CS Uni-Zap XR library"  
 /note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Confidial library. Point inoculation of Guy11 at center of oatmeal agar plate. Conidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

Query Match 0.4%; Score 19.8; DB 1; Length 27;  
 Best Local Similarity 91.3%; Pred. No. 1.2e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAAATC 1202  
 |||||

Db 3 AGAGAGAGAGAGAGAGAACTC 25

## RESULT 117

CL654516/c

LOCUS

27 bp DNA linear GSS 09-JUL-2004  
 PR10120d B08 - PR10120d.B21 (27) Note: Recurring String Mixed stage

DEFINITION

fosmid library of P. pacificus var. California Pristionchus  
 pacificus genomic, genomic survey sequence.

ACCESSION

CL654516

VERSION

GSS.

KEYWORDS

Pristionchus pacificus

SOURCE

Pristionchus pacificus

ORGANISM

Eukaryota; Metazoa; Nematoda; Diplogasterida;

REFERENCE

1 (bases 1 to 27)

AUTHORS

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE

AppADB: an ACeDB database for the nematode satellite organism

JOURNAL

Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spermatetr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seg primer: T7

Class: fosmid ends.

Location/Qualifiers

source

1. .27

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_1lb="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pBifos-5 Fosmid vector"

QY

5393 AAAAAATCAAAAAAGAAAAA 5415  
 |||||

Db 23 AAAAAATCAAAAAAGAAAAA 1

RESULT 118

A2776487

LOCUS

27 bp DNA linear GSS 16-FEB-2001  
 2M0010G08F Mouse 10kb plasmid UGCGM library Mus musculus genomic

DEFINITION

clone UGCG2M0010G08 F, genomic survey sequence.  
 A2776487

ACCESSION

A2776487

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE

1 (bases 1 to 27)

JOURNAL

Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,

COMMENT

Niederhausen,A., Rose,M., Rose,R., Stokes,R., Tinney,A., von

Unpublished (2000)

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0010 row: G column: 08

Seg primer: CGTGTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence step: 27.

Location/Qualifiers

1. .27

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG2M0010G08"

/sex="Male"

/lab\_host="G. Coli strain XL10-Gold, T1-resistant, P-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adapter oligonucleotides were

ligated to the blunt ends in high molar excess. The

digested DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1181 GAGAAAGAGAGAGAGAAATCAGAG 1206  
Db 2 GAGAGAGAGAGAGAGAGATGAG 27

RESULT 119  
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LOCUS 2M0170U19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0170U19 F, genomic survey sequence.  
ACCESSION AZ862643  
VERSION AZ862643.1 GI:13060151  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0170 row: J column: 19  
Seq primer: CCGTGTAAACACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0170U19"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5393 AAAAAATTCAAAAAGAAAAATGA 5418  
Db 26 AAAAAAAAAAAAAAAAAAAAAAAGA 1

RESULT 120  
AZ873739/c 27 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0187C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0187C08 R, genomic survey sequence.  
ACCESSION AZ873739  
VERSION AZ873739.1 GI:13082111  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0187 row: C column: 08  
Seq primer: CACACGAAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

#### FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0187C08"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1173 AGAATCAGAGAGAGAGAGAGA 1198

Db 27 AGAGCTTAGAGAGAGAGAGAGA 2

RESULT 121  
TA257B07P 27 bp DNA 1linear GSS 13-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 257b07, forward sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AL483278.1 GI:11849602  
VERSION AL483278.1 GI:11849602  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 27)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
TITLE Direct Subcloning  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhls@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaundin and B. Barrell, Oxford University Press, 1999).  
Email: nhlsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1..27  
Location/Qualifiers  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="257b07"

Query Match 0.4%; Score 19.6; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAATGAAAA 5421

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 122  
AZ430288/c 23 bp DNA 1linear GSS 03-OCT-2000  
LOCUS AZ430288  
DEFINITION 1M0214012R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
ACCESSION AZ430288  
VERSION AZ430288.1 GI:10554301  
KEYWORDS GSS.

SOURCE  
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00  
Plate: 0214 row: O column: 12  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

FEATURES  
source  
1..23  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.4; DB 1; Length 23;  
Best Local Similarity 95.2%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1180 AGAGAAAGAGAGAGAGAGAAA 1200

Db 23 AGAGAGAGAGAGAGAGAGAAA 3

RESULT 123  
AL587648 25 bp mRNA 1linear EST 02-MAR-2001  
LOCUS AL587648  
DEFINITION ROS060C07, mRNA sequence.  
ACCESSION AL587648  
VERSION AL587648.1 GI:13192682  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)

RESULT 123  
AL587648 25 bp mRNA 1linear EST 02-MAR-2001  
LOCUS AL587648  
DEFINITION ROS060C07, mRNA sequence.  
ACCESSION AL587648  
VERSION AL587648.1 GI:13192682  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)

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ORGANISM      Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
               Phasianine; Gallus.
REFERENCE      1 (bases 1 to 25)
AUTHORS        Murray, F.
TITLE          BP Chicken Brain Library
JOURNAL        Unpublished (2001)
COMMENT        Contact: Frazer Murray
               Dept. Genomics and Bioinformatics
               Roslin Institute
               Roslin, Midlothian, EH25 9PS, UK
               Tel: +44 (0)131 527 4200
               Fax: +44 (0)131 440 0434
               Email: frazer.murray@bbsrc.ac.uk
               GCGGCCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
               (*6854-
               Seq primer: M13P.
FEATURES       Location/Qualifiers
               1..25
               /organism="Gallus gallus"
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               /clone="ROS060C07"
               /tissue_type="Brain"
               /dev_stage="Unknown"
               /lab_host="DH10B"
               /clone_lib="BP Chicken Brain Library"
               /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
               unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
               5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
               GCGGCCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
               Clontech (*6854-1)"
Query Match    0.4%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATCAAAAAAGAAAAAAT 5416
Db 24 AAAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 124
A2381039      25 bp      DNA      linear      GSS 02-OCT-2000
LOCUS         1M0137N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    Clone UUGC1M0137N18 F, genomic survey sequence.
ACCESSION     A2381039
VERSION       A2381039.1 GI:10494739
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 25)
AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0137 row: N column: 18

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Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
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               /db_xref="taxon:10090"
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               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PWD42 (g14732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
Query Match    0.4%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATCAAAAAAGAAAAAAT 5416
Db 2 AAAAAAAAAAAAAAAAAAAAAAAT 25

RESULT 125
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LOCUS         1M0146A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    Clone UUGC1M0146A08 F, genomic survey sequence.
ACCESSION     A2386891
VERSION       A2386891.1 GI:10500591
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 25)
AUTHORS        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0146 row: A column: 08
               Seq primer: CGTGTAAACGACGCCAGT

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Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

FEATURES  
source

1..25  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAAGAAAAAT 5416  
Db 1 AAAAAAAAAAAAAAAAAAAAAAT 24

RESULT 126  
LOCUS AL587774/c 26 bp mRNA linear EST 02-MAR-2001  
DEFINITION AL587774 BP Chicken Brain Library Gallus gallus cDNA clone  
ACCESSION AL587774  
VERSION AL587774.1 GI:13192808  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 26)  
REFERENCE  
AUTHORS Murray P.  
TITLES BP Chicken Brain Library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@rosc.ac.uk  
GCGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (\*6854-  
46854-  
Seq primer: M13P.  
Location/Qualifiers

FEATURES  
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/db\_xref="taxon:9031"

/clone="ROS063A11"  
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/clone\_1lb="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3'; 3' adaptor sequence: 5' GCGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (\*6854-1)"

Query Match 0.4%; Score 19.2; DB 1; Length 26;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAAGAAAAAT 5416  
Db 24 AAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 127  
LOCUS R26779/c 26 bp mRNA linear EST 24-APR-1995  
DEFINITION yH44f06.g1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:132611 3' similar to gb:W85164 SERUM RESPONSE FACTOR ACCESSION YP001111 (HUMAN); mRNA sequence.  
ACCESSION R26779  
VERSION R26779.1 GI:782914  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 26)  
REFERENCE  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maier, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, B., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 1384  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LBNL  
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert length: 1384 Std Error: 0.00  
Seq primer: Promega -21m13  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1..26  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:538233"  
/db\_xref="taxon:9606"  
/clone="IMAGE:132611"  
/sex="Female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_1lb="Soares placenta Nb2HP"  
/note="Organ: placenta; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACGTGAAGATTCGCGCCGCGAGAAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors

FEATURES  
source  
1..26  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"

(pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatma Bonaldo. "

Query Match 0.4%; Score 19.2; DB 1; Length 26;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAAGAAAA 5414  
Db 24 TTTAAAAAATACAAAAAGAAAA 1

## RESULT 128

AM327923 27 bp mRNA linear EST 28-JAN-2000  
DEFINITION dr02g08.x1 NIH\_MGC\_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA  
sequence.

ACCESSION AM327923  
VERSION AM327923.1 GI:6798418  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.  
AUTHORS 1 (bases 1 to 27)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Edge Biosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILM)  
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILM at:  
www.bio.lnl.gov/bbrp/image/image.html

Plate: L1CM0029 row: M column: 16  
Seq primer: 21M13 forward primer (AB1).

FEATURES  
source Location/Qualifiers

1..27  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2847159"  
/tissue\_type="Burkitt lymphoma"  
/cell\_line="MGC4"  
/clone\_lib="NIH MGC 3"  
/note="Organ: Lymph; Vector: pOTB7a; Library prepared by  
Edge Biosystems."

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAA 5415  
Db 1 AAAAAAATACAAAAAGAAAA 27

RESULT 129  
CF291968 27 bp mRNA linear EST 14-AUG-2003  
LOCUS CF291968  
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA  
sequence.

ACCESSION CF291968  
VERSION CF291968.1 GI:33661001  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 27)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
AUTHORS Song,S.I., Kim,D.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1..27  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ROOT--02-J21"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAA 5415  
Db 27 AAAAAAATACAAAAAGAAAA 1

## RESULT 130

CF328811 27 bp mRNA linear EST 18-AUG-2003  
LOCUS CF328811  
DEFINITION NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--03-009, mRNA  
sequence.

ACCESSION CF328811  
VERSION CF328811.1 GI:33805864  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacridae; Oryzaceae; Oryza.  
1 (bases 1 to 27)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
AUTHORS Song,S.I., Kim,D.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1..27  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="NACL--03-009"  
/tissue\_type="callus"



/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT--04-N08"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1ib="AtUMT-overexpressing transgenic rice plasmid  
CDNA library (JMT)"  
/note="Vector: PCR4-TOPO, site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jaomaiolate Carboxyl  
methyltransferase overexpression line."

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134  
CN545326/C 27 bp mRNA linear EST 30-APR-2004  
LOCUS  
DEFINITION EST 17370 Green Grape Skin Triplex2 Library Vitis vinifera cDNA  
CN545326  
ACCESSION  
VERSION CN545326.1 GI:46909951  
KEYWORDS  
SOURCE  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 27)

## REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)

TITLE

JOURNAL

UMR 619 - Equipe Biologie de la Vigne  
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Fax: 00-33- (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

COMMENT

## FEATURES

source  
1..27  
Location/Qualifiers

/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00GL005G05"  
/dev\_stage="green stage"  
/clone\_1ib="Green Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 135  
CN545492 27 bp mRNA linear EST 30-APR-2004  
LOCUS  
DEFINITION EST 17436 Green Grape Skin Triplex2 Library Vitis vinifera cDNA  
clone B3CS00GL005G05 3', mRNA sequence.  
CN545492  
ACCESSION  
VERSION CN545492.1 GI:46910117  
KEYWORDS  
SOURCE  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 27)

## REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)

TITLE

JOURNAL

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Fax: 00-33- (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

COMMENT

## FEATURES

source

1..27  
Location/Qualifiers  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00GL005G05"  
/dev\_stage="green stage"  
/clone\_1ib="Green Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 136

CN545530/C

LOCUS  
DEFINITION EST 17474 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA  
clone B3CS00RL003B09 3', mRNA sequence.  
CN545530  
ACCESSION  
VERSION CN545530.1 GI:46910155  
KEYWORDS  
SOURCE  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 27)

## REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)

TITLE

JOURNAL

UMR 619 - Equipe Biologie de la Vigne  
Contact: Hamdi S.





Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
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Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

# FEATURES

source  
1..27  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00RL006H07"  
/dev\_stage="ripening stage"  
/clone\_lib="Ripe Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 140 27 bp mRNA linear EST 30-APR-2004  
LOCUS CN546052/C  
DEFINITION EST 18004 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA  
ACCESSION CN546052  
VERSION CN546052.1 GI:46910677  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
1 (bases 1 to 27)  
Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)

REFERENCE AUTHORS  
TITLE  
JOURNAL  
COMMENT  
UMR 619 - Equipe Biologie de la Vigne  
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Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

# FEATURES

source  
1..27  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00RL007H09"

/dev\_stage="ripening stage"  
/clone\_lib="Ripe Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 141 27 bp mRNA linear EST 30-APR-2004  
LOCUS CN546271/C  
DEFINITION EST 18223 Green Grape Berry Lambda Triplex2 Library Vitis vinifera  
ACCESSION CN546271  
VERSION CN546271.1 GI:46910896  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
1 (bases 1 to 27)  
Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
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Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

# REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
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Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

# FEATURES

source  
1..27  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS1XGB015C02"  
/dev\_stage="green stage"  
/clone\_lib="Green Grape Berry Lambda Triplex2 Library"  
/note="Organ: Fruit without seeds; Vector: lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 142 27 bp mRNA linear EST 30-APR-2004  
LOCUS CN546337/C  
DEFINITION EST 18289 Green Grape Berry Lambda Triplex2 Library Vitis vinifera  
ACCESSION CN546337  
VERSION CN546337.1 GI:46910962  
KEYWORDS EST.

**SOURCE**  
**ORGANISM** Vitis vinifera  
 Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
 1 (bases 1 to 27)

**REFERENCE**  
 Abbal,P., Agasee,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedalechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
 Unpublished (2002)

**TITLE**  
 UMR 619 - Equipe Biologie de la Vigne  
 Université de Bordeaux I, Institut National de la Recherche Agronomique  
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 Fax: 00-33-(0)5-57-12-25-48  
 Email: e.hamdi@bordeaux.inra.fr

**JOURNAL**  
 Unpublished (2002)

**COMMENT**  
 Contact: Hamdi S.

**FEATURES**  
 source  
 1. .27  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultiivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3CS1XGB015H08"  
 /dev\_stage="green stage"  
 /clone\_1lb="Green Grape Berry Lambda Triplex2 Library"  
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiI; Site\_2: SfiIb; Oriented library"

**Query Match**  
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 5389 AATTAAAAAATTCAAAAAGAAAAA 5415  
 |||||||  
 27 AAAAAAAAAAAAAAAAAAAAAA 1

**Db**

**RESULT 143**  
 CDS46559/c 27 bp mRNA linear EST 30-APR-2004  
 LOCUS EST 18703 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
 CDS46559  
 CDNA clone B3CS58RB008C12 3', mRNA sequence.  
 ACCESSION  
 VERSION CDS46559.1 GI:46911184  
 KEYWORDS  
 EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
 1 (bases 1 to 27)  
 Abbal,P., Agasee,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedalechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
 Unpublished (2002)

**JOURNAL**  
 Unpublished (2002)

**COMMENT**  
 Contact: Hamdi S.  
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 Tel: 00-33-(0)5-57-12-25-50  
 Fax: 00-33-(0)5-57-12-25-48  
 Email: e.hamdi@bordeaux.inra.fr  
 Seq primer: T7.

**FEATURES**  
 Location/Qualifiers  
 1. .27  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultiivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3CS58RB008C12"  
 /dev\_stage="ripe stage"  
 /clone\_1lb="Ripe Grape Berry Lambda Triplex2 Library"  
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiI; Site\_2: SfiIb; Oriented library"

**Query Match**  
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 5389 AATTAAAAAATTCAAAAAGAAAAA 5415  
 |||||||  
 27 AAAAAAAAAAAAAAAAAAAAAA 1

**Db**

**RESULT 144**  
 CDS46574/c 27 bp mRNA linear EST 30-APR-2004  
 LOCUS EST 18718 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
 CDS46574  
 CDNA clone B3CS58RB008B04 3', mRNA sequence.  
 ACCESSION  
 VERSION CDS46574.1 GI:46911199  
 KEYWORDS  
 EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
 1 (bases 1 to 27)  
 Abbal,P., Agasee,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedalechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
 Unpublished (2002)

**JOURNAL**  
 Unpublished (2002)

**COMMENT**  
 Contact: Hamdi S.  
 UMR 619 - Equipe Biologie de la Vigne  
 Université de Bordeaux I, Institut National de la Recherche Agronomique  
 71, Avenue Edouard Bourlèaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
 Tel: 00-33-(0)5-57-12-25-50  
 Fax: 00-33-(0)5-57-12-25-48  
 Email: e.hamdi@bordeaux.inra.fr  
 Seq primer: T7.

**FEATURES**  
 source  
 1. .27  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultiivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3CS58RB008B04"  
 /dev\_stage="ripe stage"  
 /clone\_1lb="Ripe Grape Berry Lambda Triplex2 Library"  
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiI; Site\_2: SfiIb; Oriented library"

**Query Match**  
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 5389 AATTAAAAAATTCAAAAAGAAAAA 5415  
 |||||||  
 27 AAAAAAAAAAAAAAAAAAAAAA 1

**Db**

**RESULT 145**

NB9936/c 27 bp mRNA linear EST 02-APR-1996  
LOCUS zB2e12.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:302926.3, similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,  
MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION NB9936  
VERSION NB9936.1 GI:1443263  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Hillier,L., Clark,N., Dubucq,T., Elliston,K., Hawking,M.,  
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaekis,E., Waterston,R., Williamson,A., Woldmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Washington University School of Medicine  
Contact: Wilson RK  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watscn.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: RT primer  
High quality sequence stop: 8.  
Location/Qualifiers  
1..27  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1247858"  
/db\_xref="taxon:9606"  
/clone="IMAGE:302926"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Toorgan: lung; Vector: pT7R3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo (dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCCCAATTTTCTTTT-3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7R3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Patima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NBHL19W."

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
DB 27 AATGCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 146  
AZ344642/c 27 bp DNA linear GSS 29-SEP-2000  
LOCUS AZ344642  
DEFINITION 1M0078H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0078H15 R, genomic survey sequence.  
ACCESSION AZ344642  
VERSION AZ344642  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niedermauern,A. and Wright,D., Weise,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0078 row: H column: 15  
Seq primer: CACACGGAACACCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1..27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0078H15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (y114732114[gb]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415  
DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 147  
AZ401672/c 27 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ401672  
DEFINITION 1M0168R04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0168R04 R, genomic survey sequence.  
ACCESSION AZ401672  
VERSION AZ401672.1 GI:10516746  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Title Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 Plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0168 row: K column: 04  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 1..27  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0168K04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;  
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAATTAATCAATTAATGAATTA 5415  
 DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 148  
 LOCUS AZ434285 27 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0220B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0220B08 R, genomic survey sequence.  
 ACCESSION AZ434285  
 VERSION AZ434285.1 GI:10558298  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 27)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Title Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 Plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0220 row: B column: 08  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 1..27  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0220B08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;  
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5398 AATACAAAAGAAAAATGAAATTA 5424  
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 149  
 LOCUS AZ458228 27 bp DNA linear GSS 04-OCT-2000  
 DEFINITION IM0262C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0262C12 F, genomic survey sequence.  
 ACCESSION AZ458228  
 VERSION AZ458228.1 GI:10616353  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

RESULT	150
AZ486791/c	
LOCUS	AZ486791.1
DEFINITION	27 bp DNA linear GSS 05-OCT-2000
ACCESSION	U0315KX21F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0315K21 F, genomic survey sequence.
VERSION	AZ486791
KEYWORDS	AZ486791.1 GI:10653911
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eumariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

RESULT	151
AZ495352/c	
LOCUS	
DEFINITION	27 bp DNA linear GSS 05-OCT-2000
ACCESSION	AZ495352
VERSION	IM033JIE1F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM033JIE1 F, genomic survey sequence.
KEYWORDS	AZ495352 AZ495352.1 GI:10670743
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scutognath; Muridae; Murinae; Mus. 1 (bases 1 to 27) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

**TITLE**  
Niederhuesern, A. and Wright, D., Weiss, R.  
**JOURNAL**  
Mouse whole genome scaffolding with paired end reads from 10kb  
**COMMENT**  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0331 row: E column: 14  
Seq primer: CCTGTGTAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

**FEATURES**  
source  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCIM031814"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.3%; Score 19; DB 1; Length 27;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 5399 ATGCAAAAAGAAAAATGAAATTA 5425  
Db 27 AAGAAAAAGAAAAAGAAAAA 1

**RESULT 152**  
A2511894/c 27 bp DNA linear GSS 05-OCT-2000  
LOCUS IM0357811F Mouse 10kb plasmid UGCM library Mus musculus genomic  
DEFINITION clone UGCM0357811 F, genomic survey sequence.  
ACCESSION A2511894  
VERSION A2511894.1 GI:10693210  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhuesern, A. and Wright, D., Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
**JOURNAL**  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: E column: 11  
Seq primer: CCTGTGTAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

**FEATURES**  
source  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCIM0357811"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.3%; Score 19; DB 1; Length 27;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 5389 AATTAAAAATTCAAAAAGAAAAA 5415  
Db 27 AAAAAAAGAAAAAGAAAAA 1

**RESULT 153**  
A2580921/c 27 bp DNA linear GSS 13-DEC-2000  
LOCUS IM0369824F Mouse 10kb plasmid UGCM library Mus musculus genomic  
DEFINITION clone UGCM0369824 F, genomic survey sequence.  
ACCESSION A2580921  
VERSION A2580921.1 GI:11695417  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhuesern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb





**COMMENT**

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0460 row: D column: 12  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Insert: 10000/1001154

## FEATURES

Location/Qualifiers

Query Match	0.34	Score 19	DB 1	Length 27
Best Local Similarity	81.54	Pred. NO. 1.6e+02		
Matches	22	Conservative	0	Mismatches 5, Indels 0, Gaps 0,
QY	5389	AAATTAAAAAATTCACAAAAACAAAAA	5415	
DB	27	AAAAAAAAAAAAAAAAAAAAAAAAA	1	

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

University of Utah Genome Center  
 1000 University of Utah

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: 0 column: 11  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid  
High quality sequence, stop: 27.

## FEATURES

**Location/Qualifiers**

```
Query Match      0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0
```

QY 5389 AATTAAATTAATTCAGAAAAAGAAAAA 5415  
|||||  
|||  
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
|||||

TITLE	Mouse whole genome scaffolding with paired end reads from 10xb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: B column: 15  
Seq primer: CGTGTGTAACGACGCGCAGT  
Class: plasmid ends  
high quality sequence stop: 27.

**FEATURES**  
**Source**

	Query Match	0.3%	Score 19;	DB 1;	Length 27;
	Best Local Similarity	81.5%;	Pred No. 1.6e+02;		
	Matches	22;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
OY	5389 AATTAAAAAATTCAGAAAACGAAAAA	5415			
Db	1 AAAAAAAAAAAAAAAAAAAAAAAAAAA	27			

RESULT	158
LOCUS	TA355B06P
DEFINITION	TA355B06P T. brucei sheared genomic DNA clone 355b06, forward sequence, genomic survey sequence.
ACCESSION	AL493923
VERSION	AL493923.1
KEYWORDS	GSS.
SOURCE	GI:11870552
ORGANISM	Trypanosoma brucei Trypanosoma brucei Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE	Trypanosoma. 1 (bases 1 to 27)
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of

*Trypanosoma brucei* (TRU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The *+* *i* method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of *T. brucei* sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/Projects/T/brucei/>.

**FEATURES**  
**SOURCE**

Query Match	0.3%	Score 19;	DB 1;	Length 27;
Best Local Similarity	81.5%;	Pred. No. 1.6e+02;		
Matches 22; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

RESULT	159
AZ382013	
LOCUS	AZ382013
DEFINITION	23 bp DNA linear GSS 02-OCT-2000 IM013M1R mouse 10kb plasmid UUCGCM library Mus musculus genomic clone UUCGIM013M14 R, genomic survey sequence.
ACCESSION	AZ382013
VERSION	AZ382013.1 GI:10495713
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 23) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Nidehausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss
JOURNAL	
COMMENT	

**FEATURES**  
**SOURCE**

```

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 90.9%; Pred. No. 1.4e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATGCAAAAAA 5414  
|||||  
Db 2 AAAAAAAAAATGCAAAAAA 23

RESULT 160  
CD43368/c 24 bp mRNA linear EST 25-JUN-2004  
LOCUS IRB8\_E10 IRB8\_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr  
DEFINITION Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.  
ACCESSION CD743368  
VERSION CD743368.1 GI:49247179  
KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.

1 (bases 1 to 24)  
Dana, A.N., Lobo, N.F., Hillenmeyer, M.E., and Collins, F.H.  
Hematophagy-associated gene expression patterns in adult female  
Anopheles gambiae mosquitoes  
Unpublished (2003)  
Contact: Dana A.N.  
Frank H. Collins Laboratory  
University of Notre Dame  
Center for Tropical Disease Research and Training, Dept. of Biol.  
Sci., Notre Dame, IN 46556, USA  
Tel: 574 - 631 - 3241  
Fax: 574 - 631 - 3996  
Email: adana@nd.edu

PCR Primers  
FORWARD: ctcgggaagcgcgcattgtgttg  
BACKWARD: atagactcactatagggcgatggc  
Seq primer: ctcgggaagcgcgcattgtgttg.  
Location/Qualifiers

#### FEATURES

1. 24  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="4Atr"  
/db\_xref="taxon:7165"  
/sex="Female"  
/tissue\_type="Abdomen"  
/dev\_stage="Female adult 5-7 days post eclosion"  
/lab\_host="R. coli XL1-Blue"  
/clone\_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr  
Abdomen Library"  
/note="Vector: lamdatrip1x2 (Clontech), Site 1: Sfi IA,  
Site 2: Sfi IB; Plasmodium berghei-infected rat blood-fed  
adult female An. gambiae mosquitoes were flash frozen  
after a 30 hour incubation of adult mosquitoes at 19  
degrees Celsius. Total RNA extracted from abdomens

separated from remaining carcass. cDNA inserts >500 bp  
cloned directionally into ltripleX2; Sfi IA site is 5'.  
Non-normalized and Non-amplified plasmid library. Single  
pass sequencing reactions from 5' end."

Query Match 0.3%; Score 18.8; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.5e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAATGCAAAAAA 5425  
|||||  
Db 23 AAAAAAAAAATGCAAAAAA 1

RESULT 161  
AZ404078 25 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M017207F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION Clone UGCG1M017207 F, genomic survey sequence.  
ACCESSION AZ404078  
VERSION AZ404078.1 GI:10528091  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)  
Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0172 row: J column: 07  
Seq primer: CCGTGTAAACGACGCCACGT  
Clas: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

#### FEATURES

1. 25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M017207"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 25;  
Best Local Similarity 90.9%; Pred. No. 1.5e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5394 AAAAAATACAAAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 162  
AZ813253 26 bp DNA linear GSS 29-FEB-2001  
LOCUS  
DEFINITION 1M0034D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0034D09 F, genomic survey sequence.

ACCESSION AZ813253  
VERSION  
KEYWORDS  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: D column: 09  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

FEATURES Location/Qualifiers

1..26

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0034D09"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 26;  
Best Local Similarity 90.9%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAAAAA 5414  
Db 4 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 163  
AZ813253 26 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0080M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0080M20 F, genomic survey sequence.

ACCESSION AZ813253  
VERSION  
KEYWORDS  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: M column: 20  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

FEATURES Location/Qualifiers

1..26

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0080M20"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 26;  
Best Local Similarity 90.9%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1180 AGAGAAAGAGAGAGAGAGAAAT 1201

Db 24 AGAGAGAGAGAGAGAGAGAT 3

RESULT 164

CF638767 25 bp mRNA linear EST 02-OCT-2003

LOCUS D06.G05 Filamentous Forced Diploid Ustilago maydis CDNA 3', mRNA  
DEFINITION sequence.

ACCESSION CF638767.1 GI:37402758

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ustilago maydis

Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

1 (bases 1 to 25)

Nugent, K.G., Choffe, K. and Saville, B.J.

Gene Expression during Ustilago maydis Diploid Filamentous Growth:

EST Library Creation and Analyses

Fungal Genet. Biol. 41 (3), 349-360 (2004)

Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utoronto.ca

Plate: UTM-UM-D126/7-006-UTM row: 05 column: G

Seq primer: T7 Reverse (5' GAGTATACGACTCATATAGG 3')

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Ustilago maydis"

/mol\_type="mRNA"

/strain="FBD12"

/db\_xref="taxon:5270"

/cell\_type="mycelia"

/dev\_stage="Filamentous diploid"

/clone\_lib="Filamentous Forced Diploid"

/note="Vector: pSport; mRNA was extracted from diploid

mycelia. A cDNA library was constructed and

unidirectionally cloned into pSPORT plasmid, with the use

of the Superscript II cDNA Library Construction Kit."

Query Match 0.3%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.6e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5393 AAAAAATACAAAAAAGAAATG 5417

Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 165

NS9260 25 bp mRNA linear EST 23-FEB-1996

LOCUS yz8d11.61 Soares multiple sclerosis 2NBHNSP Homo sapiens CDNA

DEFINITION clone IMAGE:289557 3' similar to gp:M77693 DIAMINE

ACCESSION NS9260

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

1 (bases 1 to 25)

Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,

Trevaskis, R., Waterston, R., Williamson, A., Woldmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: m13 -40 forward

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="CDB:3905397"

/db\_xref="taxon:9606"

/clone="IMAGE:289557"

/sex="male"

/tissue\_type="multiple sclerosis lesions"

/dev\_stage="Age 46"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares multiple sclerosis 2NBHNSP"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker V-TYPR: phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5']

TGTTACCAATCGAAGTGGAGCGCCGATTTTTTTTTTTTTTTT 3']

, double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT733 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M. Patricia Bonaldi. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH)."

Query Match 0.3%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.6e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5389 AATTAAAAAATACAAAAAAGAAA 5413

Db 25 AATTAAAAAATACAAAAAAGAAA 1

RESULT 166

AZ355083 26 bp DNA linear GSS 02-OCT-2000

LOCUS IM0094D14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0094D14 R, genomic survey sequence.

ACCESSION AZ355083

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT

Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0094 row: D column: 14  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0094D14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.6; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1.7e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5401 ACMAAAAGAAAAATGAAATGAA 5425

Db 1 AAAAAAAAAAAAAAAAAATRAAAAAA 25

RESULT 167  
AZ437459 26 bp DNA linear GSS 03-OCT-2000  
LOCUS AZ437459/c  
DEFINITION 1M0225B15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0225B15 R, genomic survey sequence.

ACCESSION AZ437459  
VERSION AZ437459.1 GI:10561472

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

## REFERENCE

AUTHORS

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0225 row: B column: 15  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0225B15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.6; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1.7e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAAATG 5417

Db 26 AAAAAAAAAAGAAAAAGAAAAAAG 2

RESULT 168  
AZ623156 26 bp DNA linear GSS 13-DEC-2000  
LOCUS AZ623156/c  
DEFINITION 1M0460101R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0460101 R, genomic survey sequence.

ACCESSION AZ623156  
VERSION AZ623156.1 GI:11745346

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

## REFERENCE

AUTHORS

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)



/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UNGCM library"  
/note="Vector: PWD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.4; DB 1; Length 22;  
Best Local Similarity 95.0%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1199

Db 21 AGAGAGAGAGAGAGAGAGAA 2

RESULT 171  
AJ695799/c

LOCUS AJ695799 23 bp mRNA linear EST 29-JUN-2004  
DEFINITION AJ695799 Bos taurus cDNA clone KN261-055\_007, mRNA sequence.  
ACCESSION AJ695799  
VERSION AJ695799.1 GI:49429218  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 23)  
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -mscore 20  
and -mismatch 12 options. Vector: BluescriptII(SK+) R. Site1: EcoRI  
R. Site2: SmaI 5' Seg Primer T3 Normalised library constructed from  
bovine ovary. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.airgenomics.org.  
Location/Qualifiers  
1..23  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="KN261-055\_007"  
/tissue\_type="ovary"  
/clone\_lib="KN261"  
/note="Vector: BluescriptII(SK+); Site 1: EcoRI; Site 2:  
SmaI; Single pass sequencing. Normalised library  
constructed from bovine ovary."

FEATURES  
source

Query Match

0.3%; Score 18.2; DB 1; Length 23;

Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAATACAAAAAGAAAAA 5415  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 172

AJ747297 23 bp mRNA linear EST 07-JUL-2004  
DEFINITION AJ747297 reverse - unstimulated minus stimulated macrophage Sus  
scrofa cDNA clone R\_1\_D05, mRNA sequence.

ACCESSION AJ747297  
VERSION AJ747297.1 GI:49917514  
KEYWORDS EST.

Sus scrofa (pig)  
SOURCE Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 23)  
Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.  
and Dixon, L.  
Development of a porcine cDNA microarray  
Unpublished (2004)  
Contact: Hopwood PA  
Dept. of Preclinical Veterinary Sciences  
Royal School for Veterinary Studies  
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM  
Sequencing was performed by ARK genomics. This clone is available  
from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,  
UK. See www.ark-genomics.org or contact info@arkgenomics.org.

TITLE Development of a porcine cDNA microarray  
JOURNAL Unpublished (2004)  
COMMENT

FEATURES  
source

1..23  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9623"  
/clone="R\_1\_D05"  
/tissue\_type="lung"  
/cell\_type="macrophage"  
/clone\_lib="reverse - unstimulated minus stimulated  
macrophage"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 173

CF279238 23 bp mRNA linear EST 14-AUG-2003  
LOCUS CF279238/c

DEFINITION 14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12,  
mRNA sequence.

ACCESSION CF279238  
VERSION CF279238.1 GI:33656624  
KEYWORDS EST.

Oryza sativa (japonica cultivar-group)  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriaraloideae; Oryzaceae; Oryza.

1 (bases 1 to 23)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

COMMENT



of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 320 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

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1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library (14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 174

LOCUS CP297943/C 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--01-B24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B24, mRNA sequence.

ACCESSION CP297943  
VERSION CP297943.1 GI:33669704

KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacroidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

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1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-B24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 175

LOCUS CP310501/C 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--05-C24.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--05-C24, mRNA sequence.

ACCESSION CP310501  
VERSION CP310501.1 GI:33682262

KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhacroidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

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1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-C24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsible element binding transcription factor 3 overexpression line."
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Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 176

LOCUS CP319212/C 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--09-K06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-K06, mRNA sequence.

ACCESSION CP319212  
VERSION CP319212.1 GI:33690973

KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Ehrhartoidae; Oryzae; Oryza.  
1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1..23  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HD--09-K06"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was"

treated with ABA(20um) for 1hr. Oligo-capped mRNA was"

reverse transcribed and then used for PCR. mRNA was"

derived from rice Histone Deacetylase overexpression"

line."

Query Match

Best Local Similarity 87.0%; Score 18.2; DB 1; Length 23;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAAAAAATCAAAAAAAAAA 5415

Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 178

CF322953

LOCUS

DEFINITION

HDN--02-109.g1 OshDAC1-overexpressing transgenic rice lambda phage

clone HDN--02-109, mRNA sequence.

ACCESSION

CF322953

VERSION

CF322953.1

KEYWORDS

EST.

ORIGIN

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzae; Oryza.

1 (bases 1 to 23)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1..23  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HDN--02-109"

Query Match

Best Local Similarity 87.0%; Score 18.2; DB 1; Length 23;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAAAAAATCAAAAAAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 178

CF322953

LOCUS

DEFINITION

HDN--04-D14.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone HDN--04-D14, mRNA

sequence.

ACCESSION

CF322953

VERSION

CF322953.1

KEYWORDS

EST.

ORIGIN

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzae; Oryza.

1 (bases 1 to 23)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1..23  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="NACL--04-D14"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped"

with oligoribonucleotides and then used as templates for"

RT-PCR."

Query Match

Best Local Similarity 87.0%; Score 18.2; DB 1; Length 23;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAAAAAATCAAAAAAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 179

CF322953

LOCUS

DEFINITION

HDN--04-D14.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone HDN--04-D14, mRNA

sequence.

ACCESSION

CF322953

VERSION

CF322953.1

KEYWORDS

EST.

ORIGIN

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzae; Oryza.

1 (bases 1 to 23)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

```

DEFINITION   NACL--05-B19.D1 Rice callus plasmid cDNA library (NACL) Oryza
              sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
              sequence.
ACCESSION    CF329694.1 GI:33807601
VERSION      CF329694.1
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 23)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE        JOURNAL
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.
              Location/Qualifiers
                1..23
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="NACL--05-B19"
                /tissue_type="callus"
                /dev_stage="Proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: SCORI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 TTTAAATAATACAAAGAGAAA 5413
Db 23 TTTAAATAATACAAAGAGAAA 1

RESULT 180
CF334657      23 bp mRNA linear EST 18-ANG-2003
LOCUS         JMT--04-A14.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION    library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-A14, mRNA sequence.
ACCESSION     CF334657
VERSION       CF334657.1 GI:33817648
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 23)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE        JOURNAL
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

```

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FEATURES      Location/Qualifiers
source        1..23
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="JMT--04-A14"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="AtJMT-overexpressing transgenic rice plasmid
              cDNA library (JMT)"
              /note="Vector: PCR4-TOPO; Site 1: SCORI; Oligo-capped mRNA
              was reverse transcribed and then used for PCR. mRNA was
              prepared from Arabidopsis thaliana Col-0 mature leaf
              methyltransferase overexpression line."

Query Match      0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAGAGAAA 5415
Db 1 AAAAAAATACAAAGAGAAA 23

RESULT 181
CN545940      23 bp mRNA linear EST 30-ADR-2004
LOCUS         EST 17885 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION    clone B3CS00RL006F03 3', mRNA sequence.
ACCESSION     CN545940
VERSION       CN545940.1 GI:46910565
KEYWORDS      EST.
SOURCE        Vitis vinifera
ORGANISM      Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
REFERENCE     1 (bases 1 to 23)
              Abbal,P., Agasee,A., Ageorges,A., Atanaseova,R., Barrieu,F.,
              Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimpel,J.,
              Hamdi,S., Romieu,C. and Terrier,N.
              Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
              Unpublished (2002)
TITLE        JOURNAL
COMMENT      Contact: Hamdi S.
              UMR 619 - Equipe Biologie de la Vigne
              Université de Bordeaux I, Institut National de la Recherche
              Agronomique
              71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
              France
              Tel: 00-33-(0)5-57-12-25-50
              Fax: 00-33-(0)5-57-12-25-48
              Email: s.hamdi@bordeaux.inra.fr
              Seq primer: 17.
              Location/Qualifiers
                1..23
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultivar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CS00RL006F03"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                Seta1; Site_2: Seta1B; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAGAGAAA 5415

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Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 182  
CNS46520/c 23 bp mRNA linear EST 30-APR-2004

LOCUS  
DEFINITION EST 18664 Ripe Grape Berry lambda Triplex2 library Vitis vinifera  
CNS46520  
ACCESSION CDNA clone B3C557RB007H08 3', mRNA sequence.  
CNS46520  
VERSION CNS46520.1 GI:46911145  
KEYWORDS  
SOURCE  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 23)  
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Gillesant, D., Grimplet, J.,  
Hamdi, S., Komieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

FEATURES  
source  
location/Qualifiers  
1..23  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3C557RB007H08"  
/dev\_stage="ripe stage"  
/clone\_lib="Ripe Grape Berry lambda Triplex2 library"  
/note="Organ: Fruit without seeds; Vector: Lambda  
Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 183  
COS577495/c 23 bp mRNA linear EST 20-JUN-2004

LOCUS  
DEFINITION TVEST077D06 TV30236\_PT CDNA Library Trichomonas vaginalis cDNA 5',  
mRNA sequence.  
COS577495  
ACCESSION COS577495.1 GI:50407891  
KEYWORDS  
SOURCE  
ORGANISM Trichomonas vaginalis  
Trichomonas vaginalis  
Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
1 (bases 1 to 23)  
Zhou, Y., Shu, W. M., Huang, S. C. C., Huang, K. Y. and Tang, P.  
Analysis of Gene Expression Profile in Trichomonas vaginalis by EST  
Sequencing (2003)  
Unpublished (2003)  
Contact: Tang, P.

Molecular Regulation and Bioinformatics Laboratory, College of  
Medicine  
Chang Gung University  
259 Wenhsa 1st. Road, Kweishan, Taoyuan 333, Taiwan  
Tel: +886 3 3283016 EXT5136  
Fax: +886 3 3283031  
Email: petang@mail.cgu.edu.tw  
PCR Primers  
FORWARD: T7  
BACKWARD: T3  
Seq primer: T3.

FEATURES  
source  
location/Qualifiers  
1..23  
/organism="Trichomonas vaginalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:5722"  
/cell\_line="ATCC30236"  
/dev\_stage="Trophozoites at mid-log phase"  
/lab\_host="XLI Blue-MR"  
/clone\_lib="TV30236\_PT CDNA Library"  
/note="Vector: Lambda ZAP-Express (Stratagene); Site\_1:  
EcoRI; Site\_2: XhoI"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 184  
AZ309219/c 23 bp DNA linear GSS 29-SEP-2000

LOCUS  
DEFINITION IM0013608F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0013608 F, genomic survey sequence.  
AZ309219  
ACCESSION AZ309219.1 GI:10349986  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,  
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0013 row: G column: 08  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES  
source  
location/Qualifiers  
1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0013608"  
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g1|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent B. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 185  
AZ309851 23 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0017112F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0017112 F, genomic survey sequence.  
ACCESSION AZ309851  
VERSION AZ309851.1 GI:10351256  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: L column: 12  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1. 23  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0017112"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

FEATURES  
SOURCE

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g1|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent B. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 186  
AZ312314 23 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0028006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0028006 F, genomic survey sequence.  
ACCESSION AZ312314  
VERSION AZ312314.1 GI:10356138  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0028 row: O column: 06  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0028006"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

FEATURES  
SOURCE

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 187  
A2313922/c 23 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION 1M0030A02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0030A02 R, genomic survey sequence.

ACCESSION A2313922  
VERSION A2313922.1 GI:10359299

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0030 row: A column: 02

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0030A02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 188  
A2351354 23 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION 1M0089D19P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0089D19 F, genomic survey sequence.

ACCESSION A2351354  
VERSION A2351354.1 GI:10430591

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: D column: 19

Seq primer: GGTGTAAACAGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0089D19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 189  
AZ357645 23 bp DNA linear GSS 02-OCT-2000  
LOCUS 1M0099C3P Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0099C3 P, genomic survey sequence.  
ACCESSION AZ357645  
VERSION AZ357645.1 GI:10471345  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0099 row: C column: 23  
Seq primer: CGTTGTAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

FEATURES  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0099C3"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 190  
AZ419236 23 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0195H07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
DEFINITION clone UUGCIM0195H07 R, genomic survey sequence.  
ACCESSION AZ419236  
VERSION AZ419236.1 GI:10543249  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0195 row: H column: 07  
Seq primer: CACACAGGAACACGATATAC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

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/clone="UUGCIM0195H07"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 191  
A2461220 23 bp DNA linear GSS 04-OCT-2000  
LOCUS A2461220  
DEFINITION 1M0267D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0267D05 F, genomic survey sequence.  
ACCESSION A2461220  
VERSION A2461220.1 GI:10619345  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
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Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0267 row: D column: 05  
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Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAA 5415  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 192  
A2465327 23 bp DNA linear GSS 04-OCT-2000  
LOCUS A2465327/C  
DEFINITION 1M0275K12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0275K12 F, genomic survey sequence.  
ACCESSION A2465327  
VERSION A2465327.1 GI:10623452  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
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Unpublished (2000)  
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University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0275 row: K column: 12  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

FEATURES  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA



was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 193 23 bp DNA linear GSS 04-OCT-2000  
AZ481702/c 1M0306E11P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0306E11 F, genomic survey sequence.

ACCESSION AZ481702.1 GI:10642767  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
MUS MUSCULUS

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.,

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0306 Row: B Column: 11  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 23.  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 194 23 bp DNA linear GSS 13-DEC-2000  
AZ588254/c 1M0396O24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0396O24 F, genomic survey sequence.

ACCESSION AZ588254.1 GI:11710444  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
MUS MUSCULUS

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.,

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0306 Row: O Column: 24  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 23.  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 195  
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DEFINITION 1M0405C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ593540  
VERSION AZ593540.1 GI:11715730  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0405 row: C column: 07  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES  
source Location/Qualifiers

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 196  
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DEFINITION 1M0436N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ610785  
VERSION AZ610785.1 GI:11732975  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0436 row: N column: 07  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES  
source Location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 197  
AZ647637/c 23 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0514E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0514E09 F, genomic survey sequence.  
ACCESSION AZ647637  
VERSION AZ647637.1 GI:11779301  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0514 row: B column: 09  
Seq primer: CGTGTGAAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 198  
AZ654903 23 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0529D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0529D03 R, genomic survey sequence.  
ACCESSION AZ654903  
VERSION AZ654903.1 GI:11792049  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0529 row: D column: 03  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

#### FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0529D03"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAA 23

# RESULT 199

A278751

LOCUS 23 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0014008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0014008 F, genomic survey sequence.

ACCESSION A278751  
VERSION A278751.1 GI:12908711

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

LOCUS

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0014 row: 0 column: 08

Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

# FEATURES

source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0014008"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAA 23

# RESULT 200

A2787184

LOCUS 23 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0033C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0033C07 F, genomic survey sequence.

ACCESSION A2787184  
VERSION A2787184.1 GI:12925692

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

LOCUS

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: C column: 07

Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

# FEATURES

source

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0033C07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 201  
A2792751 23 bp DNA 11linear GSS 16-FEB-2001  
LOCUS A2792751/c  
DEFINITION 2M0045K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0045K24 F, genomic survey sequence.

ACCESSION A2792751  
VERSION A2792751.1 GI:12937005

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0045 Row: K Column: 24  
Seq primer: CCGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES  
source Location/Qualifiers

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0045K24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;

Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 202  
A2859570 23 bp DNA 11linear GSS 21-FEB-2001  
LOCUS A2859570  
DEFINITION 2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0165B14 F, genomic survey sequence.

ACCESSION A2859570  
VERSION A2859570.1 GI:13054022

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0165 Row: B Column: 14  
Seq primer: CCGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES  
source Location/Qualifiers

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0165B14"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 23

# RESULT 203

AZ939608 23 bp DNA linear GSS 26-APR-2001  
LOCUS 2M0198107R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION Clone UUGC2M0198107 R, genomic survey sequence.

ACCESSION AZ939608  
VERSION AZ939608.1 GI:13800390  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE  
AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0198 row: 1 column: 07  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

source

1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0198107"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 23

# RESULT 204

BH000534 23 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0288B03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION Clone UUGC2M0288B03 R, genomic survey sequence.

ACCESSION BH000534  
VERSION BH000534.1 GI:13871760  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE  
AUTHORS  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0288 row: B column: 03  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

source

1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0288B03"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAAAAA 5415  
|||||  
23 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 205  
LOCUS TA151C02Q  
DEFINITION T. brucei sheared genomic DNA clone 151c02, reverse sequence,  
genomic survey sequence.

ACCESSION AL473028  
VERSION AL473028.1 GI:11838301  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

source  
1..23  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRU927"  
/db\_xref="taxon:5691"  
/clone="151C02"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAAAAA 5415  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 206  
LOCUS TA274B03P  
DEFINITION T. brucei sheared genomic DNA clone 274b03, forward sequence,  
genomic survey sequence.

ACCESSION AL484584  
VERSION AL484584.1 GI:11851281  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

source  
1..23  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRU927"  
/db\_xref="taxon:5691"  
/clone="274B03"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAAAAA 5415  
|||||  
23 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 207  
LOCUS TA333A10P  
DEFINITION T. brucei sheared genomic DNA clone 333a10, forward sequence,  
genomic survey sequence.

ACCESSION AL494456  
VERSION AL494456.1 GI:11870913  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
DIRECT SUBMISSION  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

#### FEATURES

source  
1..23  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRU927"  
/db\_xref="taxon:5691"  
/clone="274B03"

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

source  
1..23

/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="353a10"

Query Match 0.3%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 208  
LOCUS AM247159 24 bp mRNA linear EST 07-JUN-2000  
DEFINITION 2819627.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819627 3',  
mRNA sequence.  
ACCESSION AM247159  
VERSION AM247159.1 GI:6590152  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mhc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2819627.5prime  
Email: c9abbs-remail.nih.gov  
Contact: Robert Strausberg, Ph.D.  
Tissue Procurement: DCTP/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/bhrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu/Low Quality Sequence: 24  
contiguous PHRED high quality bases following vector sequence. Very  
low Quality Sequence: Trace file contained 24 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: L1CM2 row: B column: 12  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24

#### FEATURES

source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819627"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adapter: GGCAAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match

0.3%; Score 18.2; DB 1; Length 24;

Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAATGAATATAA 5425  
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 209  
LOCUS BG670391 24 bp mRNA linear EST 30-APR-2001  
DEFINITION DRNBAP06 Rat DRG Library Rattus norvegicus cDNA clone DRNBAP06 5',  
mRNA sequence.  
ACCESSION BG670391  
VERSION BG670391.1 GI:13892490  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
REFERENCE  
AUTHORS Kiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,  
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
Zhang,X., Chen,Z., Han,Z.G., and Zhang,X.  
Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
MEDLINE 22056133  
PUBMED 12060780

COMMENT Contact: Zhang Xu  
Laboratory of Sensory System  
Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China  
Tel: 86-21-66474870-121  
Fax: 86-21-64713446  
Email: xu.zhang@ion.ac.cn  
This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@hgc.sh.cn)  
PCR Primers  
FORWARD: T3  
BACKWARD: T7  
Seq primer: T3  
POLYA=No.  
Location/Qualifiers  
1..24

#### FEATURES

source

/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="DRNBAP06"  
/sex="male"  
/tissue\_type="dorsal root ganglion"  
/dev\_stage="adult"  
/clone\_1ib="Rat DRG Library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 210  
LOCUS BX554611 24 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX554611 Gloesina morsitans morsitans adult infected gut Gloesina  
morsitans morsitans cDNA clone Tse16d06\_pic, mRNA sequence.  
ACCESSION BX554611



VERSION BX554611.1 GI:33378684  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 24)  
 REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.  
 FEATURES  
 source  
 1..24  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse16d06\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_1fb="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"  
 Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 |||||  
 24 AAAAAAAAAAAAAAAAAAAAAA 2  
 Db  
 RESULT 211  
 CF276855 24 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--02-C19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-C19, mRNA sequence.  
 ACCESSION CF276855  
 VERSION CF276855.1 GI:33654241  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; Oryza.  
 1 (bases 1 to 24)  
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale sequencing analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 FEATURES  
 source  
 1..24  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="14ETL--02-C19"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1fb="Rice etiolated leaf plasmid cDNA library (14ETL)"  
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
 Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 |||||  
 1 AAAAAAAAAAAAAAAAAAAAAA 23  
 Db  
 RESULT 212  
 CF281313 24 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--08-F05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-F05, mRNA sequence.  
 ACCESSION CF281313  
 VERSION CF281313.1 GI:33658700  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; Oryza.  
 1 (bases 1 to 24)  
 REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale sequencing analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 FEATURES  
 source  
 1..24  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
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 /clone="14ETL--08-F05"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1fb="Rice etiolated leaf plasmid cDNA library (14ETL)"  
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
 Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5415  
 |||||  
 Db 23 AAAAAAAAAAAAAAAAAA 1

## RESULT 213

CF301561 24 bp mRNA linear EST 15-AUG-2003  
 LOCUS CF301561/c 7LEAF--06-H15.b1 Rice leaf plasmid library II (7LEAF) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--06-H15, mRNA  
 sequence.

ACCESSION CF301561  
 VERSION CF301561  
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..24  
 location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO, site 1: EcoRI; mRNA was capped  
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 RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5415  
 |||||  
 Db 24 AAAAAAAAAAAAAAAAAA 2

RESULT 214  
 CF320862 24 bp mRNA linear EST 15-AUG-2003  
 LOCUS CF320862/c HD--11-O12.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--11-O12, mRNA sequence.

ACCESSION CF320862  
 VERSION CF320862  
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

1..24  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HD--11-O12"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOPO, site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5415  
 |||||  
 Db 24 AAAAAAAAAAAAAAAAAA 2

RESULT 215  
 CN545249 24 bp mRNA linear EST 30-APR-2004  
 LOCUS CN545249/c EST 17193 Green Grape Skin Triplex2 library Vitis vinifera cDNA  
 DEFINITION clone B3CS00GL004H11 3', mRNA sequence.

ACCESSION CN545249  
 VERSION CN545249  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 24)  
 Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
 Couture, C., Dedaldechamp, F., Delrot, S., Gilsant, D., Grimplet, J.,  
 Hamdi, S., Komieu, C. and Terrier, N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
 or seeds) at Various Developmental Stages  
 Unpublished (2002)  
 Contact: Hamdi S.  
 UMR 619 - Equipe Biologie de la Vigne  
 Universite de Bordeaux I, Institut National de la Recherche  
 Agronomique  
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
 France  
 Tel: 00-33-(0)5-57-12-25-50  
 Fax: 00-33-(0)5-57-12-25-46  
 Email: s.hamdi@bordeaux.inra.fr  
 Seq primer: 17.

FEATURES  
 source

1..24  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3CS00GL004H11"

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/dev stage="green stage"
/clone_1lb="Green Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SiteA; Site_2: SiteB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 216
CN545307/c 24 bp mRNA linear EST 30-APR-2004
LOCUS EST 17251 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545307
VERSION CN545307.1 GI:46909932
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbal,P., Agase,A., Ageorges,A., Atanaseva,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/dev_stage="green stage"
/clone_1lb="Green Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SiteA; Site_2: SiteB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 217
CN545657/c 24 bp mRNA linear EST 30-APR-2004
LOCUS EST 17601 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545657
VERSION CN545657.1 GI:46910282
KEYWORDS EST.

```

```

SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbal,P., Agase,A., Ageorges,A., Atanaseva,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004E09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SiteA; Site_2: SiteB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 218
CN545784/c 24 bp mRNA linear EST 30-APR-2004
LOCUS EST 17728 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545784
VERSION CN545784.1 GI:46910409
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbal,P., Agase,A., Ageorges,A., Atanaseva,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

```

## FEATURES

Location/Qualifiers  
1..24

/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00RL005H06"  
/dev\_stage="ripening stage"  
/clone\_1lb="Ripe Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1: SfiI; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415  
|||||  
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

## RESULT 219

CNS46689/c 24 bp mRNA linear EST 30-APR-2004  
LOCUS CNS46689  
DEFINITION EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis  
vinifera cDNA clone B3CS37TB007F12 3', mRNA sequence.

ACCESSION CNS46689  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis  
vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 24)  
Abbal, F., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Gissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Université de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

## REFERENCE

AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

Location/Qualifiers  
1..24

/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
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/clone="B3CS37TB007F12"  
/dev\_stage="veraison stage"  
/clone\_1lb="Turning Grape Berry Lambda Triplex2 Library"  
/note="Organ: Fruit without seeds; Vector: Lambda  
Triplex2; Site\_1: SfiI; Site\_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415  
|||||  
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

## RESULT 220

## A2328848

LOCUS A2328848 24 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0052M17R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0052M17 R, genomic survey sequence.

ACCESSION A2328848  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Bacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiser, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0052 row: M column: 17  
Seq primer: CACACAGAAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

## REFERENCE

AUTHORS

## JOURNAL

COMMENT

## FEATURES

source

Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0052M17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (g14732114[gbl]AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 221

A2363562

LOCUS	AZ363562	24 bp	DNA	linear	GSS 02-OCT-2000
DEFINITION	IM109G10P Mouse 10kb plasmid UICM1 library Mus musculus genomic clone UICM10109610 F, genomic survey sequence.				
ACCESSION	AZ363562				
VERSION	AZ363562.1	GI:10477262			
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nidehausern,A. and Wright D.,Weise,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0. 00 Plate: 0109 row: G column: 10 Seq primer: CGTGTAAAGACGCACGAT Clas: plasmid ends High quality sequence stop: 24.				

DEFINITION	IM0145D02R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0145D02 R, genomic survey sequence.
ACCESSION	AZ386491
VERSION	AZ386491.1
KEYWORDS	GI:10500191
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus. Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Petersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genomic Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0145 row: D column: 02 Seq primer: CACACGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24. Location/Qualifiers
FEATURES	

	0.3%	Score 18.2	DB 1	Length 24
Query Match Similarity	87.0%	Pred. No.	1.7e+02	
Best Local Similarity	0	Mismatches	3	Indels
Matches	20	Conservative		Gaps
Oy	5393	AAAAAAAAATCAAAAAAGAAAAA	5415	
D6	1	AAAAAAAAAAAAAAAAAAAAAAAAAA	23	
RESULT 222				
AZ386491				
LOCUS	AZ386491	24 bp	DNA	linear
				GSS 02-OCT-2000

Query Match	0.3%	Score 18.2	DB 1	Length 24
Best Local Similarity	87.0%	Prod. No. 1.7e+02		
Matches 20	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	5393	AAAAAAAAATCAGAAAAAGAAAAA	5415	
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	23	
RESULT 223				
AZ390642/c				
LOCUS	AZ390642			
DEFINITION	IM0155H07F Mousee 10kb plasmid DUGC1M library Mus musculus genomic	24 bp	DNA	linear GSS 03-OCT-2000

	0.3%	Score 18.2	DB 1	Length 24
Query Match Similarity	87.0%	Pred. No.	1.7e+02	
Best Local Similarity	0	Mismatches	3	Indels
Matches	20	Conservative		Gaps
Oy	5393	AAAAAAAAATCAAAAAAGAAAAA	5415	
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAA	23	
RESULT 222				
AZ386491			24 bp	DNA
LOCUS	AZ386491			linear GSS 02-OCT-2000

Query Match	0.3%	Score 18.2	DB 1	Length 24
Best Local Similarity	87.0%	Prod. No. 1.7e+02		
Matches 20	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	5393	AAAAAAAAATCAGAAAAAGAAAAA	5415	
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	23	
RESULT 223				
AZ390642/c				
LOCUS	AZ390642			
DEFINITION	IM0155H07P Mousee 10kb plasmid DUGC1M library Mus musculus genomic	24 bp	DNA	linear GSS 03-OCT-2000

accession clone UGCG1M0152H07 F, genomic survey sequence.  
 version AZ390642  
 keywds AZ390642.1 GI:10505685  
 source GSS  
 organism Mus musculus (house mouse)  
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 24)  
 authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 journal Unpublished (2000)  
 comment Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 tel: 801 585 5606  
 fax: 801 585 7177  
 email: ddunn@genetics.utah.edu  
 insert length: 10000 Std Error: 0.00  
 plate: 0152 row: H column: 07  
 seq primer: CGTTGTAAACGACGCGCAGT  
 class: plasmid ends  
 high quality sequence stop: 24.  
 features location/Qualifiers  
 source 1..24  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0152H07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAAA 5415  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 224  
 AZ438069 24 bp DNA linear GSS 03-OCT-2000  
 LOCUS AZ438069  
 DEFINITION 1M0228A10F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 accession clone UGCG1M0228A10 F, genomic survey sequence.

accession AZ438069  
 version AZ438069.1 GI:10562178  
 keywds GSS.  
 source Mus musculus (house mouse)  
 organism Mus musculus  
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 24)  
 authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 journal Unpublished (2000)  
 comment Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 tel: 801 585 5606  
 fax: 801 585 7177  
 email: ddunn@genetics.utah.edu  
 insert length: 10000 Std Error: 0.00  
 plate: 0228 row: A column: 10  
 seq primer: CGTTGTAAACGACGCGCAGT  
 class: plasmid ends  
 high quality sequence stop: 24.  
 features location/Qualifiers  
 source 1..24  
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 /db\_xref="taxon:10090"  
 /clone="UGCG1M0228A10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAAAAGAAAAAAT 5416  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAT 23

RESULT 225  
 AZ458112 24 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ458112/C  
 DEFINITION 1M0261F24R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 accession clone UGCG1M0261F24 R, genomic survey sequence.

VERSION AZ458112.1 GI:10616237  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0261 row: E Column: 24  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
 /clone="UUC1M0261E24"  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAAATGAAATAAA 5425  
 DB 23 AAAAAAAAAAATGAAATAAA 1

RESULT 226  
 AZ459280/c 24 bp DNA linear GSS 04-OCT-2000  
 LOCUS IM0264A05F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 DEFINITION Clone UUC1M0264A05 F, genomic survey sequence.  
 ACCESSION AZ459280  
 VERSION AZ459280.1 GI:10617405

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0264 row: A Column: 05  
 Seq primer: CGTTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1..24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0264A05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAATGAAATAAA 5415  
 DB 24 AAAAAAAAAAATGAAATAAA 2

RESULT 227  
 AZ621257/c 24 bp DNA linear GSS 13-DEC-2000  
 LOCUS IM0454E23F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 DEFINITION Clone UUC1M0454E23 F, genomic survey sequence.  
 ACCESSION AZ621257  
 VERSION AZ621257.1 GI:11743447  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0454 row: B column: 23  
Seq primer: CCTCTTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0454E23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAAATGAAATATAA 5425  
|||||  
Db 24 AAAAAAAAAAATGAAATATAA 2

RESULT 228  
AZ644621/c 24 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION 1M0508F12R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0508F12 R, genomic survey sequence.  
ACCESSION AZ644621  
VERSION AZ644621.1 GI:11773331  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0508 row: F column: 12  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0508F12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415  
|||||  
Db 24 AAAAAAAAAAAGAAAAA 2

RESULT 229  
AZ786257 24 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M003H11R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M003H11 R, genomic survey sequence.  
ACCESSION AZ786257  
VERSION AZ786257.1 GI:12923835  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus



REFERENCE  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE  
Unpublished (2000)

JOURNAL  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: H column: 11  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0031H11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415  
|||||  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 230  
LOCUS AZ834990 24 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0129A05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0129A05 F, genomic survey sequence.  
ACCESSION AZ834990  
VERSION AZ834990.1 GI:13004898  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE  
Unpublished (2000)

JOURNAL  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: A column: 05  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

FEATURES  
source  
1. 24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0129A05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 231  
LOCUS AZ970038 24 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0243J02F Mouse 10kb plasmid UUCG2M library Mus musculus genomic clone UUCG2M0243J02 F, genomic survey sequence.  
ACCESSION AZ970038  
VERSION AZ970038.1 GI:13841265  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0243 row: J column: 02  
Seq primer: CGTGTAAAACGACGGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0243J02"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 232  
AZ984490 24 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0266H05F Mouse 10kb plasmid UUCG2M library Mus musculus genomic  
DEFINITION clone UUCG2M0266H05 F, genomic survey sequence.  
ACCESSION AZ984490  
VERSION AZ984490.1 GI:13855717  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0266 row: H column: 05  
Seq primer: CGTGTAAAACGACGGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0266H05"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.7e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 233  
AZ993423 24 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0278019F Mouse 10kb plasmid UUCG2M library Mus musculus genomic  
DEFINITION clone UUCG2M0278019 F, genomic survey sequence.  
ACCESSION AZ993423  
VERSION AZ993423.1 GI:13864650  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

**TITLE**  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingay, A., von  
 Niederhuser, A. and Wright, D., Weis, R.  
**JOURNAL**  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 Plasmid inserts  
 Unpublished (2000)  
**COMMENT**  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0278 row: 0 column: 19  
 Seq primer: CGTTGTAAACGACGCGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 24.

**FEATURES**  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0278019"  
 /sex="Female"  
 /lab\_host="R. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: pMD42nv. Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent R. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**Query Match**  
 Best Local Similarity 0.3%; Score 18.2; DB 1; Length 24;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 ||||| ||||| ||||| ||||| |||||  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

**RESULT 234**  
 TA169D12P/C 24 bp DNA 1linear GSS 13-DEC-2000  
**LOCUS**  
 T. brucei sheared genomic DNA clone 169d12, forward sequence,  
**DEFINITION**  
 genomic survey sequence.  
**ACCESSION**  
 AL478922  
**VERSION**  
 AL478922.1 GI:11840452  
**KEYWORDS**  
 GSS.  
**SOURCE**  
 Trypanosoma brucei  
 Trypanosoma brucei  
**ORGANISM**  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
**REFERENCE**  
 1 (bases 1 to 24)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Ackin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

**TITLE**  
**JOURNAL**

**COMMENT**

Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submissions  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nhle@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nhle@sanger.ac.uk  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

**FEATURES**  
 source  
 1..24  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TRU927"  
 /db\_xref="taxon:5691"  
 /clone="169d12"

**Query Match**  
 Best Local Similarity 0.3%; Score 18.2; DB 1; Length 24;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 ||||| ||||| ||||| ||||| |||||  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

**RESULT 235**  
 TA27B08Q 24 bp DNA 1linear GSS 13-DEC-2000  
**LOCUS**  
 T. brucei sheared genomic DNA clone 27b08, reverse sequence,  
**DEFINITION**  
 genomic survey sequence.  
**ACCESSION**  
 AL453584  
**VERSION**  
 AL453584.1 GI:11850982  
**KEYWORDS**  
 GSS.  
**SOURCE**  
 Trypanosoma brucei  
 Trypanosoma brucei  
**ORGANISM**  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
**REFERENCE**  
 1 (bases 1 to 24)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Ackin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 Direct Submissions  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nhle@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nhle@sanger.ac.uk  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

**FEATURES**  
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 1..24  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TRU927"

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/db_xref="taxon:5691"
/clone="37D08"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 236
TA354C06P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 354c06, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION     AL494439.1 GI:11870896
VERSION       GSS.
KEYWORDS      Trypanosoma brucei
SOURCE        Trypanosoma brucei
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE      1 (bases 1 to 24)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
                Rockville, MD. Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                to give a tight size distribution (
                4 kb). The v + 1 method used for the library construction is
                described in detail in Smith, H. and Venter, J.C. (Making small
                insert libraries for whole genome shotgun sequencing projects. In
                Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                Barrell, Oxford University Press, 1999).
                Email: nelsayed@tigr.org
                Details of T. brucei sequencing at the Sanger Centre are available
                at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source          1..24
                /organism="Trypanosoma brucei"
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                /db_xref="taxon:5691"
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Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 237
TA371F11P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 371f11, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION     AL495622
VERSION       AL495622.1 GI:11871906
KEYWORDS      GSS.
SOURCE        Trypanosoma brucei
ORGANISM      Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

```

```

Trypanosoma.
1 (bases 1 to 24)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
                Rockville, MD. Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                to give a tight size distribution (
                4 kb). The v + 1 method used for the library construction is
                described in detail in Smith, H. and Venter, J.C. (Making small
                insert libraries for whole genome shotgun sequencing projects. In
                Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                Barrell, Oxford University Press, 1999).
                Email: nelsayed@tigr.org
                Details of T. brucei sequencing at the Sanger Centre are available
                at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source          1..24
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                /clone="371f11"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 238
TA95B08P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 95b08, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION     AL459003
VERSION       AL459003.1 GI:11861374
KEYWORDS      GSS.
SOURCE        Trypanosoma brucei
ORGANISM      Trypanosoma brucei
                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE      1 (bases 1 to 24)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
                Rockville, MD. Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                to give a tight size distribution (
                4 kb). The v + 1 method used for the library construction is
                described in detail in Smith, H. and Venter, J.C. (Making small
                insert libraries for whole genome shotgun sequencing projects. In
                Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                Barrell, Oxford University Press, 1999).
                Email: nelsayed@tigr.org
                Details of T. brucei sequencing at the Sanger Centre are available
                at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
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/clone\_11b="Rice root plasmid cDNA library (14ROO7)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 242  
CP299288  
LOCUS 7LEAF--03-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--03-B01, mRNA  
sequence.  
ACCESSION CP299288  
VERSION CP299288.1 GI:33671049  
KEYWORDS EST  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

ACCESSION CP299288  
VERSION CP299288.1 GI:33671049  
KEYWORDS EST  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..25  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/clone\_11b="Rice leaf plasmid cDNA library II (7LEAF)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 243  
CF300333/c  
LOCUS 7LEAF--04-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--04-L02, mRNA  
sequence.  
ACCESSION CF300333  
VERSION CF300333.1 GI:33672094  
KEYWORDS EST.

ACCESSION CF300333  
VERSION CF300333.1 GI:33672094  
KEYWORDS EST.

SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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/organism="Oryza sativa (japonica cultivar-group)"  
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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 244  
CF301712/c  
LOCUS 7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--06-K21, mRNA  
sequence.  
ACCESSION CF301712  
VERSION CF301712.1 GI:33673473  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
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ACCESSION CF301712  
VERSION CF301712.1 GI:33673473  
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ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

/clone="7LEAF--06-K21"  
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Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415  
DB 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 245 CF316323/c 25 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--05-H05.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--05-H05, mRNA sequence.  
CF316323  
CF316323  
ACCESSION CF316323.1 GI:3368084  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source

1. .25  
/organism="Oryza sativa (japonica cultivar-group)"  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415  
DB 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 246 CF317714/c

LOCUS CF317714 25 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--07-103.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--07-103, mRNA sequence.  
CF317714  
CF317714  
ACCESSION CF317714.1 GI:33689475  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .25  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415  
DB 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 247 CF319073/c 25 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--09-H05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--09-H05, mRNA sequence.  
CF319073  
CF319073  
ACCESSION CF319073.1 GI:33690834  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 25)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1..25 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"  
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/clone\_1ib="OSHDA1-overexpressing transgenic rice plasmid  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 248

CF330786/c 25 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--06-K11.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--06-K11, mRNA  
sequence.

ACCESSION CF330786.1 GI:33809794

VERSION CF330786

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
TITLE Oryza sativa (japonica cultivar-group)  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 25)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1..25 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"  
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Query Match 0.3%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 249

CNS45505/c 25 bp mRNA linear EST 30-APR-2004

LOCUS EST 17449 Green Grape Skin Triplex2 library Vitis vinifera cDNA  
clone B3CS00GL005H06 3', mRNA sequence.

ACCESSION CNS45505

VERSION CNS45505.1 GI:46910130

KEYWORDS EST.

SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
TITLE Vitis vinifera  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 25)

REFERENCE 1  
Abbal, P., Agasse, A., Ageorges, A., Aranasova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Komieu, C. and Terrier, N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: 17.

FEATURES  
source

1..25 Location/Qualifiers

/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00GL005H06"  
/dev\_stage="green stage"  
/clone\_1ib="Green Grape Skin Triplex2 library"  
/note="Organ: Fruit skin; Vector: lambda Triplex2; Site\_1:  
5'fla; Site\_2: 3'fla; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 250

CNS46041/c 25 bp mRNA linear EST 30-APR-2004

LOCUS EST 17993 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA  
clone B3CS00RL007G10 3', mRNA sequence.

ACCESSION CNS46041

VERSION CNS46041.1 GI:46910666

KEYWORDS EST.

SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
TITLE Vitis vinifera  
JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 25)

Query Match 0.3%; Score 18.2; DB 1; Length 25;



AUTHORS	Abbal, P., Agassese, A., Ageorges, A., Atanasova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
FEATURES	source 1. 25 /organism="Vitis vinifera" /mol_type="mRNA" /db_xref="taxon:29760" /clone="B3CS00RL007G10" /dev_stage="ripening stage" /clone_1lb="Ripe Grape Skin Triplex2 Library" /note="Organ: Fruit Skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match	0.3%; Score 18.2; DB 1; Length 25; Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	5393 AAAAAAAAAACAAAAAGAAAAA 5415                         25 AAAAAAAAAAAAAAAAAAAAAA 3
Db	25 AAAAAAAAAAAAAAAAAAAAAA 3
RESULT 251	CNS46397 25 bp mRNA linear EST 30-APR-2004
LOCUS	EST 18350 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION	cDNA clone B3CS1XGB016B10 3', mRNA sequence.
ACCESSION	CNS46397
VERSION	CNS46397.1 GI:46911022
KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis. 1 (bases 1 to 25) Abbal, P., Agassese, A., Ageorges, A., Atanasova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002) Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
FEATURES	source 1. 25 /organism="Vitis vinifera" /mol_type="mRNA" /db_xref="taxon:29760" /clone="B3CS57RB007D09 3" /dev_stage="ripening stage" /clone_1lb="Ripe Grape Berry Lambda Triplex2 Library" /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match	0.3%; Score 18.2; DB 1; Length 25; Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	5393 AAAAAAAAAACAAAAAGAAAAA 5415                         25 AAAAAAAAAAAAAAAAAAAAAA 3
Db	25 AAAAAAAAAAAAAAAAAAAAAA 3
RESULT 252	CNS46477 25 bp mRNA linear EST 30-APR-2004
LOCUS	EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION	cDNA clone B3CS57RB007D09 3', mRNA sequence.
ACCESSION	CNS46477
VERSION	CNS46477.1 GI:46911102
KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis. 1 (bases 1 to 25) Abbal, P., Agassese, A., Ageorges, A., Atanasova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002) Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
FEATURES	source 1. 25 /organism="Vitis vinifera" /mol_type="mRNA" /db_xref="taxon:29760" /clone="B3CS57RB007D09 3" /dev_stage="ripening stage" /clone_1lb="Ripe Grape Berry Lambda Triplex2 Library" /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match	0.3%; Score 18.2; DB 1; Length 25; Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	5393 AAAAAAAAAACAAAAAGAAAAA 5415                         25 AAAAAAAAAAAAAAAAAAAAAA 3
Db	25 AAAAAAAAAAAAAAAAAAAAAA 3
RESULT 253	CNS46728 25 bp mRNA linear EST 30-APR-2004
LOCUS	EST 18499 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION	cDNA clone B3CS98TB008B03 3', mRNA sequence.
ACCESSION	CNS46728
VERSION	CNS46728.1 GI:46911353

**KEYWORDS** EST.  
**SOURCE** Vitis vinifera  
**ORGANISM** Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
**REFERENCE** 1 (bases 1 to 25)  
**AUTHORS** Abbal, P., Agasse, A., Ageorges, A., Atanaseva, R., Barlieu, F., Coure, C., Dedaldechamp, F., Delrot, S., Glessant, D., Grimpel, J., Hamdi, S., Romeu, C. and Terrier, N.  
**TITLE** Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
**JOURNAL** Unpublished (2002)  
**COMMENT** UMR 619 - Equipe Biologie de la Vigne  
 Université de Bordeaux I, Institut National de la Recherche Agronomique  
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
 Tel: 00-33- (0)5-57-12-25-50  
 Fax: 00-33- (0)5-57-12-25-48  
 Email: s.hamdi@bordeaux.inra.fr  
 Seq primer: 17:  
 Location/Qualifiers  
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 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3C38TB008B03"  
 /dev\_stage="veraison stage"  
 /clone\_lib="Turning Grape Berry Lambda Triplex2 Library"  
 /note="Organ: Fruit without seeds; Vector: Lambda  
 Triplex2; Site\_1: SflrI; Site\_2: SfiIb; Oriented library"

**Query Match** 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 5393 AAAAAATCAAAAAAGAAAA 5415  
**Db** 25 AAAAAAAAAAAAAAAAAAAAA 3

**RESULT 254**  
**LOCUS** N33150 25 bp mRNA linear EST 10-JAN-1996  
**DEFINITION** YY06G01.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270480 3' similar to gb:U29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);, mRNA sequence.  
**ACCESSION** N33150  
**VERSION** N33150.1 GI:1153549  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
**REFERENCE** 1 (bases 1 to 25)  
**AUTHORS** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
**TITLE** The Mashu-Merck EST Project  
**JOURNAL** Unpublished (1995)  
**COMMENT** Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1

**Source: IMAGE Consortium, LML.**  
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lln.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: ml3 -40 forward  
 High quality sequence stop: 1.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3880122"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:270480"  
 /sex="Male"  
 /tissue\_type="melanocyte"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares melanocyte 2NbhM"  
 /note="Vector: pTR73 (pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGACATTTTCTTTTCTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR73 vector (pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

**Query Match** 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 5393 AAAAAATCAAAAAAGAAAA 5415  
**Db** 25 AAAAAAAAAAAAAAAAAAAAA 3

**RESULT 255**  
**LOCUS** AZ344725 25 bp DNA linear GSS 29-SEP-2000  
**DEFINITION** 1M0078124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0078124 R, genomic survey sequence.  
**ACCESSION** AZ344725  
**VERSION** AZ344725.1 GI:10423962  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 25)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0078 row: 1 column: 24  
 Seq primer: CACACGAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 25.  
 Location/Qualifiers  
 1..25  
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/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0078124"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 256  
 AZ350777/c 25 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0088A04R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0088A04 R, genomic survey sequence.

ACCESSION AZ350777  
 VERSION AZ350777.1 GI:10430014  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0088 row: A column: 04  
 Seq primer: CACACAGAAACGATATGAC  
 Class: plasmid ends  
 High quality sequence stop: 25.

FEATURES  
 source 1..25  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0088A04"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 257  
 AZ389458 25 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0150B06F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0150B06 F, genomic survey sequence.

ACCESSION AZ389458  
 VERSION AZ389458.1 GI:10503166  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0150 row: B column: 06  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 25.

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

/db\_xref="taxon:10090"  
 /clone="UUGC1M0150B06"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_11b="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAAAAA 5415  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 258  
 AZ609234/c 25 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0433H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0433H19 R, genomic survey sequence.  
 ACCESSION AZ609234  
 VERSION AZ609234.1 GI:11731424  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0433 row: H column: 19  
 Seq primer: CACACAGAAACAGCTATACG  
 Class: plasmid ends  
 High quality sequence stop: 25.

FEATURES

source

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"

/clone="UUGC1M0433H19"  
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 /clone\_11b="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAAAAA 5415  
 ||||| ||||| ||||| ||||| |||||  
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 259  
 AZ623157/c 25 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0460L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0460L02 R, genomic survey sequence.  
 ACCESSION AZ623157  
 VERSION AZ623157.1 GI:11745347  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0460 row: L column: 02  
 Seq primer: CACACAGAAACAGCTATACG  
 Class: plasmid ends  
 High quality sequence stop: 25.

FEATURES

source

1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0460L02"

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

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RESULT 260
LOCUS AZ788646/c 25 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M00351L19R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M00351L9 R, genomic survey sequence.
ACCESSION AZ788646
VERSION AZ788646.1 GI:12928656
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: L column: 19
Seq primer: CACACGAGAAACGCTATAC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M00351L9"
/sex="Male"

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

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```

RESULT 261
LOCUS AZ832800/c 25 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0113M21F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0113M21 F, genomic survey sequence.
ACCESSION AZ832800
VERSION AZ832800.1 GI:13002708
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0113 row: M column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0113M21"
/sex="Male"

```

```

FEATURES
source
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0113M21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

```

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male); was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415  
|||||

Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 262  
A2949287 25 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0212008R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0212008 R, genomic survey sequence.  
ACCESSION A2949287  
VERSION A2949287.1 GI:13820514  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0212 row: O column: 08  
Seq primer: CACACAGAAACAGCTATACAC  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0212008"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female); was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415  
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 263  
A2980407 25 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0257M19 F, genomic survey sequence.  
ACCESSION A2980407  
VERSION A2980407.1 GI:13851634  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0257 row: M column: 19  
Seq primer: CGTGTAAACAGCAGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0257M19"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0257M19"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 264  
LOCUS TA154D03P/c 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 154d03, forward sequence,  
genomic survey sequence.  
ACCESSION AL472971  
VERSION AL472971.1 GI:11838244  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 25)  
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S. E., Rajandream, M. A. and Barrell, B. G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J. C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source  
1..25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="154d03"

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAACAAAAAGAAAAAT 5416  
|||||  
Db 25 AAAAAAAAAAAAAAAAAAAAAAT 3

RESULT 265  
LOCUS TA324B10P/c 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 324e10, forward sequence,  
genomic survey sequence.  
ACCESSION AL493396  
VERSION AL493396.1 GI:11867761  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 25)  
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S. E., Rajandream, M. A. and Barrell, B. G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

## COMMENT

Constructd at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J. C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1..25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="324e10"

Query Match 0.3%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
|||||  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 266  
LOCUS AJ659204 26 bp mRNA linear EST 28-UTN-2004  
DEFINITION AJ659204 KN277 Sus scrofa cDNA clone C0005215\_B14, mRNA sequence.  
ACCESSION AJ659204  
VERSION AJ659204.1 GI:4934335  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Anderson, S. I., Finlayson, H. A. and Archibald, A. L.  
TITLE Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
CONTACT: Anderson SI

Genomics and Bioinformatics

Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mnscore 20 and -mismatch 12 options. Vector: BluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arts.genomics.org.

FEATURES  
source  
location/Qualifiers

1..26  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005215.B14"  
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/clone\_1ib="KM277"  
/note="Vector: pBluescriptII(SK+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 267  
AM327613/c 26 bp mRNA linear EST 28-JUN-2000  
LOCUS dqt01b09.y1 NIH\_MGC\_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA  
DEFINITION sequence.  
ACCESSION AM327613  
VERSION AM327613.1 GI:6798108  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 26)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Edge Biosystems  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Plate: LHC80028 row: C column: 17  
Seq primer: M13R1 reverse primer (ABT).  
location/Qualifiers

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2846536"  
/issue\_type="T cell leukemia"  
/cell\_line="MGC2"  
/clone\_1ib="NIH\_MGC\_2"  
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Bdge Biosystems."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 268  
BM658913/c 26 bp mRNA linear EST 27-FEB-2002  
LOCUS LOC602768282.R1 CSEQFLX36 fetal brain Sus scrofa cDNA, mRNA  
DEFINITION sequence.

ACCESSION BM658913  
VERSION BM658913.1 GI:18959184  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 26)  
NotI; Site 2: EcoRI; sequence 5' of the insert  
(5'-NNN...NNNinsert)  
GCCAATGACACTCCACCGCGTGGCGCGGCTGAG. sequence 3' of the insert (AAGAAATTCGATTCAGCTTATCATCTGACTGAG.)  
non-normalized library, sequenced 3' with M13R primer.

REFERENCE  
AUTHORS Adelson,D.L. and Gill,C.A.  
TITLE Porcine ESTs  
JOURNAL Unpublished (2002)  
CONTACT: David L. Adelson  
Animal Breeding and Genetics  
Texas A&M University  
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
USA  
Tel: 9798452616  
Fax: 9798456970  
Email: david.adelson@tamu.edu.

FEATURES  
source  
location/Qualifiers

1..26  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/dev\_stage="fetal"  
/clone\_1ib="CSEQFLX36 fetal brain"  
/note="Organ: brain; Vector: pBluescript SK+; Site\_1: NotI; Site 2: EcoRI; sequence 5' of the insert  
(5'-NNN...NNNinsert)  
GCCAATGACACTCCACCGCGTGGCGCGGCTGAG. sequence 3' of the insert (AAGAAATTCGATTCAGCTTATCATCTGACTGAG.)  
non-normalized library, sequenced 3' with M13R primer."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
DB 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 269  
BX563414/c 26 bp mRNA linear EST 10-OCT-2003  
LOCUS BX563414 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse66e05\_p1c, mRNA sequence.

ACCESSION BX563414  
VERSION BX563414.1 GI:33430654  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriaman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes



JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW

All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source Location/Qualifiers

1..26  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:37546"  
 /clone="Tae6605\_plc"  
 /issue\_type="adult infected gut"  
 /clone\_1ib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 Db 23 AAAAAAAAAACAAAAAGAAAAA 1

RESULT 270  
 CF278359/c 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D22,  
 mRNA sequence.

ACCESSION CF278359  
 VERSION CF278359.1 GI:33655745

SOURCE EST.  
 Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarctidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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/clone\_1ib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
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 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 Db 26 AAAAAAAAAACAAAAAGAAAAA 4

RESULT 271  
 CF282426 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--09-P01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,  
 mRNA sequence.

ACCESSION CF282426  
 VERSION CF282426.1 GI:33659813

KEYWORDS EST.  
 Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarctidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)

Song,S.I., Kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 /issue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="B.colli DH10B"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415  
 Db 1 AAAAAAAAAACAAAAAGAAAAA 23

RESULT 272  
 CF296851/c 26 bp mRNA linear EST 14-AUG-2003  
 LOCUS 30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--07-G13, mRNA  
 sequence.

ACCESSION CF296851

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VERSION      CF296851.1 GI:33665884
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
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                /issue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAAA 5415
        ||||| ||||| ||||| |||||
        26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 273
CF297087      26 bp      mRNA      linear      EST 14-AUG-2003
LOCUS      30DS--07-L18.b1 Rice leaf plasmid cDNA library I (30DS) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 30DS--07-L18, mRNA
               sequence.
ACCESSION      CF297087
VERSION      CF297087.1 GI:33666120
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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                /mol_type="mRNA"

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/cultivar="Nackdong"
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/issue_type="leaf"
/dev_stage="30 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library I (30DS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAAA 5415
        ||||| ||||| ||||| |||||
        26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 274
CF299701/c      26 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N03, mRNA
               sequence.
ACCESSION      CF299701
VERSION      CF299701.1 GI:33671462
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1..26
                /organism="Oryza sativa (japonica cultivar-group)"
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAAA 5415
        ||||| ||||| ||||| |||||
        26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 275
CF302874/c      26 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      CF302874

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DEFINITION 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (japonica cultivar-group) cDNA clone 7LEAF--08-M19, mRNA sequence.

ACCESSION CF302874

VERSION CF302874.1 GI:33674635

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..26  
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/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OR 5393 AAAAAATACAAAAAGAAAAA 5415  
|||||  
26 AAAAAAAAAAAAAAAAAAAAAA 4

DB

RESULT 276  
CF311369 26 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) *Oryza sativa* (japonica cultivar-group) cDNA clone

DEFINITION ABF--06-J01, mRNA sequence.

ACCESSION CF311369

VERSION CF311369.1 GI:33683130

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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1..26  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OR 5393 AAAAAATACAAAAAGAAAAA 5415  
|||||  
26 AAAAAAAAAAAAAAAAAAAAAA 4

DB

RESULT 277  
CF311439 26 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) *Oryza sativa* (japonica cultivar-group) cDNA clone NACL--07-J02, mRNA sequence.

DEFINITION NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) *Oryza sativa* (japonica cultivar-group) cDNA clone NACL--07-J02, mRNA sequence.

ACCESSION CF311439

VERSION CF311439.1 GI:33811097

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..26  
/organism="Oryza sativa (japonica cultivar-group)"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OR 5393 AAAAAATACAAAAAGAAAAA 5415

Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 278  
CF337311/c 26 bp mRNA linear EST 18-AUG-2003

DEFINITION  
JMT--07-L06.g1 ACJMT-overexpressing transgenic rice plasmid CDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--07-L06, mRNA sequence.

ACCESSION  
CF337311 GI:33823014

VERSION  
EST.

KEYWORDS  
Oryza sativa (japonica cultivar-group)

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 26)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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1..26  
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred.No.1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 24 AAAAAAAAAAAAAAAAAAGAAAAA 2

RESULT 279  
CN545213/c 26 bp mRNA linear EST 30-APR-2004

LOCUS  
CN545213/c

DEFINITION  
EST 17457 Green Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00G1004B11 3', mRNA sequence.

ACCESSION  
CN545213

VERSION  
CN545213.1 GI:46909668

KEYWORDS  
EST.

SOURCE  
Vitis vinifera

ORGANISM  
Vitis vinifera

DEFINITION  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE  
1 (bases 1 to 26)  
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.

TITLE  
JOURNAL  
COMMENT  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: 17.

FEATURES  
source  
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/clone\_lib="Green Grape Skin Triplex2 Library"  
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred.No.1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 280  
CN545225/c 26 bp mRNA linear EST 30-APR-2004

LOCUS  
CN545225/c

DEFINITION  
EST 17169 Green Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00G1004F11 3', mRNA sequence.

ACCESSION  
CN545225

VERSION  
CN545225.1 GI:46909680

KEYWORDS  
EST.

SOURCE  
Vitis vinifera

ORGANISM  
Vitis vinifera

DEFINITION  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE  
1 (bases 1 to 26)  
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: 17.

FEATURES  
source  
1..26  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS00G1004F11"  
/dev\_stage="green stage"  
/clone\_lib="Green Grape Skin Triplex2 Library"

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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SflIA; Site_2: SflIB; Oriented library"
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Query Match	0.3%	Score 18.2;	DB 1;	Length 26;
Best Local Similarity	87.0%;	Pred. No. 1.9e+02;		
Matches 20;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	5393	AAAAAAAAATACAAAAAAGAAAAAA	5415
Db	26	AAAAAAAAAAAAAAAAAAAAAAAAAAA	4

RESULT 261	CN545546	26 bp	mRNA	linear	EST 30-APR-2004
CN545546/c	EST 17490	Ripe Grape Skin	Tridplex Library	Vitis vinifera cDNA	
LOCUS	clone B3CG08RL003D01	3'	mRNA sequence.		
DEFINITION					
DESCRIPTION					

TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hamdi S. ...

France  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
Tél: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bourseaux.inra.fr  
Seq primer: 77.../0-3151

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 5393 AAAAAAAAAAGAAAAA 5415
      ||||| ||||| |||||
Db 26 AAAAAAAAAAAAAAAAAA 4
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RESULT 282	CN545723/C	26 bp	mRNA	linear	EST 30-APR-2004
LOCUS	CN545723				
DEFINITION	EST 17667 Grape Skin Trid1ex2 library				
	clone B3CGS08RL005C03 3', mRNA sequence.				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.

TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hamdi S. <a href="mailto:h.said@agr.mcgill.ca">h.said@agr.mcgill.ca</a>

FEATURES	Location/Qualifiers
source	1. .26

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/dev_stg4e="ripening stg4e"
/clone_1b="ripe Grape Skin TripleX2 Library"
/note="Organ: Fruit skin; Vector: Lambda TripleX2; Site_1:
St1A; Site_2: St1b; Oriented library"

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QY 5393 AAAAAAAAAAGAAAAA 541
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Db 25 AAAAAAAAAAAAAAAAAA 3
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RESULT	283
CN545888/C	
LOCUS	CN545888
DEFINITION	EST 17832 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL006A07 3', mRNA sequence.
FEATURES	26 bp .     mRNA        linear     EST 30-APR-2004

REFERENCES  
1 (bases 1 to 26)  
Abdel, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F., ...

**FEATURES**  
**Source**  
 Email: [s.handi@bordeaux.inra.fr](mailto:s.handi@bordeaux.inra.fr)  
 Seq primer: T7.  
 Location/Qualifiers  
 1. .26

```

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A07"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 284
CN546608/c 26 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS58RB008H03 3', mRNA sequence.
ACCESSION CN546608
VERSION CN546608.1 GI:46911233
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
location/Qualifiers
1..26
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008H03"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 285
CN546649/c 26 bp mRNA linear EST 30-APR-2004
LOCUS CN546649/c 26 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS58RB008H03 3', mRNA sequence.
ACCESSION CN546649
VERSION CN546649.1 GI:46911234
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
location/Qualifiers
1..26
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007C08"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 286
AZ342914/c 26 bp DNA linear GSS 29-SEP-2000
LOCUS AZ342914/c 26 bp DNA linear GSS 29-SEP-2000
DEFINITION M0076C22P Mouse 10kb plasmid UGCI1M library Mus musculus genomic
clone UGCI1M0076C22 F, genomic survey sequence.
ACCESSION AZ342914
VERSION AZ342914.1 GI:10420628
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

DEFINITION EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera CDNA clone B3CS37TB007C08 3', mRNA sequence.
ACCESSION CN546649
VERSION CN546649.1 GI:46911274
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
location/Qualifiers
1..26
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007C08"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 286
AZ342914/c 26 bp DNA linear GSS 29-SEP-2000
LOCUS AZ342914/c 26 bp DNA linear GSS 29-SEP-2000
DEFINITION M0076C22P Mouse 10kb plasmid UGCI1M library Mus musculus genomic
clone UGCI1M0076C22 F, genomic survey sequence.
ACCESSION AZ342914
VERSION AZ342914.1 GI:10420628
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0076 row: C column: 22  
 Seq primer: CAGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.

## FEATURES

source

1.26  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0076C22"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PMD22ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAAATC 1202

DB 24 AGAGAGAGAGAGAGAGAGATTC 2

## RESULT 287

AZ359871 26 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0102H23R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGCLM0102H23 R, genomic survey sequence.

ACCESSION AZ359871  
 VERSION AZ359871.1 GI:10473571

## KEYWORDS

## SOURCE

## ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0102 row: H column: 23  
 Seq primer: CAGCAGGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.

## FEATURES

source

1.26  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0102H23"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PMD22ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## Query Match

Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAAAA 5415

DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 288

AZ376664 26 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0130B08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGCLM0130B08 R, genomic survey sequence.

ACCESSION AZ376664  
 VERSION AZ376664.1 GI:10490364

## KEYWORDS

## SOURCE

## ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)

## REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islem, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished (2000)

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: B column: 08  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0150D13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 289

AZ389765

LOCUS 26 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0150D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0150D13 R, genomic survey sequence.

ACCESSION

AZ389765

VERSION AZ389765.1 GI:10503473

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: D column: 13  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0150D13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 290

AZ414673

LOCUS 26 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0189M07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0189M07 F, genomic survey sequence.

ACCESSION

AZ414673

VERSION AZ414673.1 GI:10538686

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu



Plate: 0189 row: M column: 07  
 Seq primer: CGTGTGTAACACGCGCAGT  
 Class: plasmid ends  
 High quality sequence strop: 26.  
 Location/Qualifiers

## FEATURES

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 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
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QY 5393 AAAAAATACAAAAAGAAAAA 5415  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 291

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 DEFINITION clone UUGC1M0404E16 R, genomic survey sequence.  
 ACCESSION AZ593300  
 VERSION AZ593300.1 GI:11715490  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddun@genetics.utah.edu  
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 Plate: 0404 row: B column: 16

Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence strop: 26.  
 Location/Qualifiers

## FEATURES

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 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 292

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 LOCUS 1M0439E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0439E17 R, genomic survey sequence.  
 ACCESSION AZ612722  
 VERSION AZ612722.1 GI:11734912  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weis  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddun@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0439 row: B column: 17  
 Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers  
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/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

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DEFINITION clone UUC1M046307 F, genomic survey sequence.  
ACCESSION A2624441  
VERSION A2624441.1 GI:11746631  
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE Mus musculus

REFERENCE 1 (bases 1 to 26)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0463 row: G column: 07  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers  
source

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/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 294  
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DEFINITION clone UUC1M0474H08 F, genomic survey sequence.  
ACCESSION A2627846  
VERSION A2627846.1 GI:11750132  
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE Mus musculus

REFERENCE 1 (bases 1 to 26)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0474 row: H column: 08  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends

High quality sequence stop: 26.

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Location/Qualifiers  
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/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
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26 AAAAAAAAAAAAAAAAAAAAAA 4

Db  
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DEFINITION clone UUCGM0493G18 F, genomic survey sequence.  
ACCESSION A2635695.1 GI:11757885  
VERSION A2635695.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
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High quality sequence stop: 26.  
Location/Qualifiers

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/sex="Male"  
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/clone\_1lb="Mouse 10kb plasmid UUCGM library"  
/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 26;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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25 AAAAAAAAAAAAAAAAAAAAAA 3

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DEFINITION clone UUCGM0525H15 R, genomic survey sequence.  
ACCESSION A2652515  
VERSION A2652515.1 GI:11789108  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

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/sex="Male"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 AAAAAAAAAAAAAAAAAA 23

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LOCUS  
DEFINITION 2M058623F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M058623 F, genomic survey sequence.

ACCESSION  
A2800453  
VERSION  
A2800453.1 GI:12952583  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

AUTHORS  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
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JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss

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84112, USA

TEL: 801 585 5606  
FAX: 801 585 7177  
Email: ddunn@genetics.utah.edu

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Plate: 0058 row: 0 column: 23

Seq primer: CGTGTAAAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers

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/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||  
DB 26 AAAAAAAAAAAAAAAAAA 4

RESULT 298  
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LOCUS  
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clone UUCG2M0233N01 F, genomic survey sequence.

ACCESSION  
A2963974  
VERSION  
A2963974.1 GI:13835201  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

AUTHORS  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
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plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss

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84112, USA

TEL: 801 585 5606  
FAX: 801 585 7177  
Email: ddunn@genetics.utah.edu

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Class: plasmid ends

High quality sequence stop: 26.  
Location/Qualifiers

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FEATURES  
source

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/clone\_lib="Mouse 10kb plasmid UGGCM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

## RESULT 299

TA324D07P

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

SOURCE

FEATURES

source

1.26

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

Location/Qualifiers

1.26

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

Location/Qualifiers

1.26

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

Location/Qualifiers

1.26

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="TREU927"

Location/Qualifiers

1.26

/db\_xref="taxon:5691"  
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Query Match 0.3%; Score 18.2; DB 1; Length 26;  
Best Local Similarity 87.0%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

## RESULT 300

BX548564/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

source

1.21

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse101903\_p1c"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

Location/Qualifiers

1.21

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse101903\_p1c"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

Location/Qualifiers

1.21

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse101903\_p1c"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

Location/Qualifiers

1.21

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse101903\_p1c"

/issue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

Location/Qualifiers

1.21

ACCESSION A2394897  
 VERSION A2394897.1 GI:10509969  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddun@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0158 row: H column: 11  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers  
 1..21  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0158H11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200  
 |||||  
 DB 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 302  
 A2486776/c 21 bp DNA linear GSS 05-OCT-2000  
 LOCUS A2486776  
 DEFINITION 1M0315M10F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0315M10 F, genomic survey sequence.  
 ACCESSION A2486776

VERSION A2486776.1 GI:10653882  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddun@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0315 row: M column: 10  
 Seq primer: CTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0315M10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5395 AAAAATACAAAAAGAAAAA 5415  
 |||||  
 DB 21 AAAAATAAAAA 1

RESULT 303  
 A2589098 21 bp DNA linear GSS 13-DEC-2000  
 LOCUS A2589098  
 DEFINITION 1M0397B19R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0397B19 R, genomic survey sequence.  
 ACCESSION A2589098  
 VERSION A2589098.1 GI:11711288

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0397 row: B column: 19  
Seq primer: CACACAGAAACGCTATGACG  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0397B19"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200  
DB 1 AGAGAGAGAGAGAGAGAGA 21

RESULT 304  
AZ597932/c 21 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0412D23F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0412D23 F, genomic survey sequence.  
ACCESSION AZ597932  
VERSION AZ597932.1 GI:11720122  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Place: 0412 row: D column: 23  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0412D23"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5395 AAAATACAAAAAGAAAAA 5415  
DB 21 AAAAAGAAAAAGAAAAA 1

RESULT 305  
AZ627978 21 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0476104F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0476104 F, genomic survey sequence.  
ACCESSION AZ627978  
VERSION AZ627978.1 GI:11750168  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0476 row: 1 column: 04  
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Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1..21  
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/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAAA 1200  
|||||  
Db 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 306  
AZ822825 21 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0096120F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M0096120 F, genomic survey sequence.  
ACCESSION AZ822825  
VERSION AZ822825.1 GI:12992733  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: 1 column: 20  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0096120"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAACAAAAA 21

RESULT 307  
AZ633751 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M048911F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M048911 F, genomic survey sequence.  
ACCESSION AZ633751  
VERSION AZ633751.1 GI:11755941  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)

## TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: 1 column: 11  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

## source

Location/Qualifiers  
1..22

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0489111"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD29v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200  
|||||

Db 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 308  
AZ822888 23 bp DNA 1linear GSS 20-FEB-2001  
LOCUS 2M009606R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC2M009606 R, genomic survey sequence.  
ACCESSION AZ822888  
VERSION AZ822888.1 GI:1292796  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 23)

## TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: 6 column: 06  
Seq primer: CACACGAAACGATGAC  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

## source

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M009606"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD29v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 23;  
Best Local Similarity 90.5%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200  
|||||

Db 2 AGAGAGAGAGAGAGAGAGA 22

RESULT 309  
AZ627850 24 bp DNA 1linear GSS 13-DEC-2000  
LOCUS 1M0474N20F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M0474N20 F, genomic survey sequence.  
ACCESSION AZ627850  
VERSION AZ627850.1 GI:11750136  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0474 row: N column: 20  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0474N20"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent B. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 24;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5413  
||||| |||||||  
Db 4 AAAAAAAAAATAAAAA 24

RESULT 310  
AU247142 25 bp mRNA linear EST 22-APR-2004  
LOCUS AU247142 FL Lolium multiflorum cDNA clone FL023C10-5, mRNA  
DEFINITION  
ACCESSION AU247142  
VERSION AU247142.1 GI:46504411  
KEYWORDS  
SOURCE Lolium multiflorum (Italian ryegrass)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Poeeae; Lolium.  
REFERENCE  
1 (bases 1 to 25)

AUTHORS  
Ikeda,S.  
TITLE  
Lolium multiflorum EST Project  
JOURNAL  
Unpublished (2004)  
COMMENT  
Contact: Seishi Ikeda  
Japan Grassland Farming Forage Seed Association (JPSA)  
Forage Crop Research Institute (FCRI)  
Higashitakada 388-5, Nishinasuno, Tochigi 329-2742, Japan  
Tel: 81-287-37-6755  
Fax: 81-287-37-6757  
Email: siked67@fjass.or.jp  
contact:Tadaaki Takamizo (takamizo@frcr.go.jp)  
National Institute of Livestock and Grassland Science, Nishinasuno  
Resistance gene analog.  
Location/Qualifiers  
1..25  
/organism="Lolium multiflorum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4521"  
/clone="FL023C10-5"  
/tissue\_type="Inflorescence"  
/clone\_lib="PL"

Query Match 0.3%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1181 GAGAAAGAGAGAGAGAAAT 1201  
||||| |||||||  
Db 2 GAGAGAGAGAGAGAGAGACT 22

RESULT 311  
CD028814 25 bp mRNA linear EST 07-MAY-2003  
LOCUS mgc8009xp04.f.b Magnaporthe grisea CS Uni-Zap XR library Magnaporthe  
DEFINITION  
ACCESSION CD028814  
VERSION CD028814.1 GI:30410270  
KEYWORDS  
SOURCE  
ORGANISM  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 25)  
Ebbbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhattarai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
JOURNAL  
COMMENT  
Contact: Ebbbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person;  
PCR primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgc8009 row: P column: 04  
Seq primer: T3.  
Location/Qualifiers  
1..25  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgc8009xp04"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="conidia"  
/clone\_lib="Magnaporthe grisea CS Uni-Zap XR library"

/note="Vector: pbluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Confidat library. Point inoculation of Guy11 at center of oatmeal agar plate. Candida were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredfrap version 991019 and trimmed according to pnd files (0.05) and for vector segs."

Query Match 0.3%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1181 GAGAAAGAGAGAGAGAAAT 1201  
DB 2 GAGAGAGAGAGAGAGAGAACT 22

RESULT 312  
AZ510124 25 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0534K22F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG1M0534K22 F, genomic survey sequence.  
ACCESSION AZ510124  
VERSION AZ510124.1 GI:10691440  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: K column: 22  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

FEATURES  
source 1.25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0534K22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number indelible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapored mouse DNA was annealed to adapored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGGAAAGAGAGAGAGAAA 1200  
DB 25 AGGAGAGAGAGAGAGAGAGA 5

RESULT 313  
AZ659095 25 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0536E18F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG1M0536E18 F, genomic survey sequence.  
ACCESSION AZ659095  
VERSION AZ659095.1 GI:11796241  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0536 row: B column: 18  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers

FEATURES  
source 1.25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0536E18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 2;

Qy 1180 AGAGAAAGAGAGAGAGAAA 1200  
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Db 3 AGAGAGAGAGAGAGAGAGAGA 23

RESULT 314  
AZ664804 25 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0545H24F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION  
ACCESSION AZ664804  
VERSION AZ664804.1 GI:11801950  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse);  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0545 row: H column: 24  
Seq primer: CATTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.

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source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0545H24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 2;

Qy 1180 AGAGAAAGAGAGAGAGAAA 1200  
|||  
Db 25 AGAGAGAGAGAGAGAGAGAGA 5

RESULT 315  
AZ399663 24 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0165C10R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION  
ACCESSION AZ399663  
VERSION AZ399663.1 GI:10514737  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse);  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0165 row: C column: 10  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

#### FEATURES

source

1. .24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0165C10"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5402 CAAAAAGAAAAATGAAAAATGAA 5425  
||||| ||||| ||||| ||||| |||||  
Db 24 CAAAAAGAAAAATGAAAAATGAA 1

RESULT 316  
AZ514388/c 24 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0361H04 F, genomic survey sequence.  
ACCESSION AZ514388  
VERSION AZ514388.1 GI:10695704  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genomic Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: H column: 04  
Seq primer: CATTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

#### FEATURES

1. 24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361H04"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5394 AAAAAATCAAAAAAGAAAAATG 5417  
||||| ||||| ||||| ||||| |||||  
Db 24 AAAAAATCAAAAAAGAAAAATG 1

RESULT 317  
AZ607198 24 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0429G03 R, genomic survey sequence.  
ACCESSION AZ607198  
VERSION AZ607198.1 GI:11729388  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genomic Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0429 row: G column: 03  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers

#### FEATURES

1. 24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0429G03"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5392 TAAATAATACAAAAAGAAAAA 5415  
Db 1 TAAATAAAAAAAAAAAAAAAAA 24

## RESULT 318

AZ626101/c 24 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0466C07P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0466J07 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
GSS.  
AZ626101.1 GI:11748291

Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0466 row: J column: 07  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

Location/Qualifiers

FEATURES  
source  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0466J07"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gblAP129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5396 AAAATACAAAAAGAAAAATGAA 5419  
Db 24 AAAAAGAAAAAAAAAAAAAAAAA 1

## RESULT 319

AZ814559 24 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0082P18P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0082P18 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
GSS.  
AZ814559.1 GI:12984467

Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: P column: 18  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

Location/Qualifiers

FEATURES  
source  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0082P18"  
/sex="Male"  
/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gblAP129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to



and selected for ampicillin resistance."

Query Match 0.3%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGA 1198  
DB 19 AGAGAGAGAGAGAGAGA 1

RESULT 322  
AZ433566/C

LOCUS 20 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0219C02R Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
clone UGCCIM0219C02 R, genomic survey sequence.

ACCESSION AZ433566  
VERSION AZ433566.1 GI:10557579

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss  
University of Utah Genome Center

Address: 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00  
Plate: 0219 row: C column: 02

Seq primer: CACACAGGAACACGCTATACG

Class: plasmid ends

High quality sequence stop: 20.

FEATURES  
source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0219C02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGA 1198  
DB 20 AGAGAGAGAGAGAGAGA 2

RESULT 323  
AZ492997/C

LOCUS 20 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0327K24F Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
clone UGCCIM0327K24 F, genomic survey sequence.

ACCESSION AZ492997  
VERSION AZ492997.1 GI:10666247

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss  
University of Utah Genome Center

Address: 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00  
Plate: 0327 row: K column: 24

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES  
source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0327K24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCCIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."



Query Match 0.3%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198  
 |||||  
 DB 19 AGAGAGAGAGAGAGAGAGA 1

RESULT 324  
 A2770557 20 bp DNA 11linear GSS 16-FEB-2001  
 LOCUS A2770557  
 DEFINITION 1M0572N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 accession clone UUGC1M0572N08 F, genomic survey sequence.  
 VERSION A2770557  
 KEYWORDS A2770557.1 GI:12891863  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)

REFERENCE  
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plates: 0572 row: N column: 08  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

FEATURES  
 source 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0572N08"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match

0.3%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198  
 |||||  
 DB 19 AGAGAGAGAGAGAGAGAGA 1

RESULT 325  
 AJ649983 22 bp mRNA 1linear EST 07-JUL-2004  
 LOCUS AJ649983 CSEORAN19 Sus scrofa cDNA clone C0003274\_A22, mRNA  
 DEFINITION sequence.  
 accession AJ649983  
 VERSION AJ649983.1 GI:49326828  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE  
 AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
 Development of cDNA and EST resources for studying reproduction and  
 embryo development in pigs and cattle  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.020425.c. Vector identified by cross match with the -minscore 20  
 and -mismatch 12 options. Vector: pBluescriptII(ks) R. Site1: EcoRI  
 R. Site2: NotI 5' Seq Primer M13 Normalised library constructed  
 from pooled ovaries. Clones available from UK Centre for Functional  
 Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
 EH25 9PS, www.atk-genomics.org.  
 Location/Qualifiers

FEATURES  
 source 1..22  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0003274\_A22"  
 /issue\_type="ovary"  
 /clone\_lib="CSEORAN19"  
 /note="Vector: pBluescriptII(ks); Site 1: EcoRI; Site 2:  
 NotI; Single pass sequencing; Normalised library  
 constructed from pooled ovaries"

Query Match 0.3%; Score 17.4; DB 1; Length 22;  
 Best Local Similarity 94.7%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 CTGGAGCCAGCAGCCCG 49  
 |||||  
 DB 1 CTGGAGCCAGCAGCCCG 19

RESULT 326  
 AJ747407 22 bp mRNA 1linear EST 07-JUL-2004  
 LOCUS AJ747407  
 DEFINITION AJ747407 forward - stimulated minus unstimulated macrophage Sus  
 accession scrofa cDNA clone F\_C0001825b\_A06, mRNA sequence.  
 VERSION AJ747407.1 GI:49917653  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE  
 AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 1 (bases 1 to 22)  
 Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.  
 and Dixon, L.  
 Development of a porcine cDNA microarray

JOURNAL Unpublished (2004)  
 COMMENT Contact: Hopwood PA  
 Dept. of Preclinical Veterinary Sciences  
 Royal School for Veterinary Studies  
 Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM  
 Sequencing was performed by ARK genomics. This clone is available  
 from ARK-Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,  
 UK. See [www.ark-genomics.org](http://www.ark-genomics.org) or contact [info@arkgenomics.org](mailto:info@arkgenomics.org).

FEATURES  
 source  
 1..22  
 Location/Qualifiers

/organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9623"  
 /clone="F\_C0001825B\_A06"  
 /issue\_type="lung"  
 /cell\_type="macrophage"  
 /clone\_1lb="forward - stimulated minus unstimulated  
 macrophage"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAAA 5414  
 ||||| ||||| ||||| |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 327  
 AL038477 22 bp mRNA linear EST 06-UTL-2004  
 LOCUS DKF2P566C1646.r1.566 (synonym: hfkdx) Homo sapiens cDNA clone  
 DEFINITION DKF2P566C1646, mRNA sequence.  
 ACCESSION AL038477  
 AL038477.1 GI:49682139  
 EST.  
 VERSION Homo sapiens (human)  
 KEYWORDS Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 22) Ootenwaelder, B., Mewes, H.W., Gassenhuber, J. and  
 Wilmann, S.  
 TITLE EST (Ootenwaelder, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
 Location/Qualifiers

FEATURES  
 source  
 1..22  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKF2P566C1646"  
 /issue\_type="kidney"  
 /dev\_stage="fetal"  
 /lab\_host="X1-2blue"  
 /clone\_1lb="566 (synonym: hfkdx2)"  
 /note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAAGAAA 5412  
 ||||| ||||| ||||| |||||  
 Db 1 TTTAAAAAATACAAAAAGAAA 22

RESULT 328  
 AW332181/C 22 bp mRNA linear EST 31-JAN-2000  
 LOCUS AW332181  
 DEFINITION SSC7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION AW332181  
 VERSION AW332181.1 GI:6828538  
 KEYWORDS EST.  
 SOURCE Pneumocystis carinii  
 ORGANISM Pneumocystis carinii  
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
 Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 22)  
 Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,  
 Edman, J.C., Kovacs, J., and Cushion, M.  
 TITLE Expressed sequence tags from Pneumocystis carinii  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY  
 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: [staben@pop.uky.edu](mailto:staben@pop.uky.edu).  
 Location/Qualifiers

FEATURES  
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/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
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 sacrificed on 3/17/99) at Cincinnati VA facilities.  
 Trizol extracted RNA. Oligo dt priming, standard  
 conditions described by vendor, Stratagene. Further  
 details see [www.uky.edu/Project/Pneumocystis/](http://www.uky.edu/Project/Pneumocystis/)"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
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QY 5393 AAAAAAATACAAAAAGAAAA 5414  
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 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 329  
 AW332399 22 bp mRNA linear EST 31-JAN-2000  
 LOCUS AW332399/C  
 DEFINITION S842 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
 ACCESSION AW332399  
 AW332399.1 GI:6828756  
 EST.  
 VERSION Homo sapiens (human)  
 KEYWORDS Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 22)  
 Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,  
 Edman, J.C., Kovacs, J., and Cushion, M.  
 TITLE Expressed sequence tags from Pneumocystis carinii  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY  
 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: [staben@pop.uky.edu](mailto:staben@pop.uky.edu).  
 Location/Qualifiers

FEATURES  
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 /lab\_host="E. coli"

/clone lib="AGS-1"  
 /note="Vector: Lambda ZAP II; Site 1: BclRI; Site 2: XhoI;  
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 sacrificed on 3/17/99) at Cincinnati VA facilities.  
 trizol extracted RNA. Oligo dt priming, standard  
 conditions described by vendor, Stratagene. Further  
 details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
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 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414  
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 330 22 bp mRNA linear EST 15-AUG-2003  
 CF299342 7LEAF--03-P06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 LOCUS sativa (japonica cultivar-group) cDNA clone 7LEAF--03-P06, mRNA  
 DEFINITION

ACCESSION CF299342 GI:33671103  
 VERSION CF299342  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarctideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--03-P06"  
 /issue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="R.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

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QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414  
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 331 22 bp mRNA linear EST 15-AUG-2003  
 CF300133 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 LOCUS sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G19, mRNA  
 DEFINITION

ACCESSION CF300133 GI:33671894  
 VERSION CF300133  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarctideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers

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 /lab\_host="R.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
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 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414  
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 332 22 bp mRNA linear EST 15-AUG-2003  
 CF310366 ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 LOCUS library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 DEFINITION ABF--04-P14, mRNA sequence.

ACCESSION CF310366 GI:33682127  
 VERSION CF310366  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarctideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
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/mol_type="mRNA"
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/rissue_type="leaf"
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/clone_1lb="ABF3-overexpressing transgenic rice plasmid
CDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAATACAAAAAGAAAA 5414  
 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 333  
 CF311269 22 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--06-G21.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
 DEFINITION 1library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
 ABF--06-G21, mRNA sequence.  
 ACCESSION CF311269  
 VERSION CF311269.1 GI:33683030  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzaeae; Oryza.  
 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

FEATURES  
 source

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAATACAAAAAGAAAA 5414

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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 334  
 CF311713 22 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--07-B13.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
 DEFINITION 1library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
 ABF--07-B13, mRNA sequence.  
 ACCESSION CF311713  
 VERSION CF311713.1 GI:33683474  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzaeae; Oryza.  
 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /clone\_1lb="ABF3-overexpressing transgenic rice plasmid  
 CDNA library (ABF)"  
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 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

FEATURES  
 source

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5393 AAAAAATACAAAAAGAAAA 5414  
 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 335  
 CF312498 22 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--08-E15.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
 DEFINITION 1library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
 ABF--08-E15, mRNA sequence.  
 ACCESSION CF312498  
 VERSION CF312498.1 GI:33684259  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzaeae; Oryza.  
 1 (bases 1 to 22)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE  
Journal  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 336  
CF330679/c

LOCUS NACL--06-H22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--06-H22, mRNA  
sequence.

ACCESSION CF330679 GI:33809583

VERSION CF330679.1  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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## FEATURES

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methyltransferase overexpression line."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 337  
CF334430/c

LOCUS JMT--02-F04.g1 ACUMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--02-F04, mRNA sequence.

ACCESSION CF334430.1 GI:33815154

VERSION CF334430.1  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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methyltransferase overexpression line."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 338  
CF334781/c

LOCUS JMT--04-D05.g1 ACUMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--04-D05, mRNA sequence.

ACCESSION CF334781

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VERSION      CF334781.1 GI:33817904
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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        /lab_host="E.coli DH10B"
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              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
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        22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 339
LOCUS      CF336250
DEFINITION JMT--06-D20.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-D20, mRNA sequence.
ACCESSION  CF336250
VERSION     CF336250.1 GI:33820891
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultiyar="Nackdong"
        /db_xref="taxon:39947"
        /clone="JMT--08-B11"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH10B"
        /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
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        22 AAAAAAAAAAAAAAAAAAAAAA 1

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VERSION      CF337580
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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        /clone="JMT--08-B11"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH10B"
        /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
              was reverse transcribed and then used for PCR. mRNA was
              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
        ||||| ||||| ||||| |||||
        22 AAAAAAAAAAAAAAAAAAAAAA 1

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Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 341  
CF338524/C 22 bp mRNA linear EST 18-AUG-2003  
LOCUS RCL1-01-P07.g1 Regenerated callus lambda phage CDNA library (RCL1)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1-01-P07,  
mRNA sequence.  
ACCESSION CF338524 GI:33825436  
VERSION CF338524.1  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Bharitoidae; Oryzaceae; Oryza.  
1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
1..22  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="RCL1-01-P07"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_1lb="Regenerated callus lambda phage CDNA library (RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: Sct1; Site 2: Xho1; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with Sct1 and 3' end with Xho1 site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414  
|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 342  
CN545550 22 bp mRNA linear EST 30-APR-2004  
LOCUS EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA  
DEFINITION clone B3CS00RL003005 3', mRNA sequence.  
ACCESSION CN545550  
VERSION CN545550.1 GI:46910175  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; Vitaceae; Vitis.  
1 (bases 1 to 22)  
Abbal,P., Agasee,A., Ageorges,A., Atanasova,R., Barrieu,P.,  
Couture,C., Dedalechamp,F., Delrot,S., Gilsant,D., Gimpel,J.,  
Hamdi,S., Romieu,C. and Terrier,N.

TITLE  
JOURNAL  
COMMENT  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche Agronomique  
71, Avenue Edouard Bourlaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

FEATURES  
source  
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/organism="Vitis vinifera"  
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/db\_xref="taxon:29760"  
/clone="B3CS00RL003005"  
/dev\_stage="ripening stage"  
/clone\_1lb="Ripe Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1: Sct1; Site\_2: Sct1B; Oriented library"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414  
|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 343  
AZ310066 22 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0018D18R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0018D18 R, genomic survey sequence.  
ACCESSION AZ310066 GI:10351682  
VERSION AZ310066  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamdi,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0018 row: D column: 18  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence scop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

TITLE  
JOURNAL  
COMMENT  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0018 row: D column: 18  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence scop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UUGC1M0018D18"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGGAAAA 5414

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 344

AZ351527

LOCUS 22 bp DNA linear GSS 29-SEP-2000  
DEFINITION M0089507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0089507 R, genomic survey sequence.

ACCESSION

AZ351527

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNIVERSITY

RM. 308, Biomedical

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Plate: 0089

Row: B

Column: 07

Seq primer: CACACGGAACAGCATATAC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0089507"

/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGGAAAA 5414

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

## RESULT 345

AZ357630

LOCUS 22 bp DNA linear GSS 02-OCT-2000  
DEFINITION M00999M15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0099M15 F, genomic survey sequence.

ACCESSION

AZ357630

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNIVERSITY

RM. 308, Biomedical

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Plate: 0099

Row: M

Column: 15

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0099M15"

/sex="Male"



/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 346  
AZ388103 22 bp DNA linear GSS 02-OCT-2000  
LOCUS 1M0147N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0147N14 R, genomic survey sequence.  
ACCESSION AZ388103  
VERSION AZ388103.1 GI:10501811  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0147 row: N column: 14  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0147N14"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 347  
AZ401908 22 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0168P24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0168P24 R, genomic survey sequence.  
ACCESSION AZ401908  
VERSION AZ401908.1 GI:10516982  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0168 row: P column: 24  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. 22  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0168P24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 348  
A2424307 22 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M020324R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0203A24 R, genomic survey sequence.  
ACCESSION A2424307  
VERSION A2424307.1 GI:10548320  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0203 row: A column: 24  
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Classes: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/organism="Mus musculus"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 349  
A2428818 22 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0212A05 R, genomic survey sequence.  
ACCESSION A2428818  
VERSION A2428818.1 GI:10552831  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0212 row: A column: 05  
Seq primer: CACACAGAAACGCTATGACC  
Classes: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACCAAAAAA 5414  
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DB 22 AAAAAAAAAACCAAAAAA 1

RESULT 350  
AZ459654/c 22 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0264G12 R, genomic survey sequence.  
ACCESSION AZ459654  
VERSION AZ459654.1 GI:10617779  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weis, R.  
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Unpublished (2000)  
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University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0264 row: G column: 12  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. 22

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACCAAAAAA 5414  
|||||  
DB 22 AAAAAAAAAACCAAAAAA 1

RESULT 351  
AZ459654/c 22 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0264G12 R, genomic survey sequence.  
ACCESSION AZ459654  
VERSION AZ459654.1 GI:10617779  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weis, R.  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0264 row: G column: 12  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. 22

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/db\_xref="taxon:10090"  
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/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414  
|||||  
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 352  
A2463503/c 22 bp DNA linear GSS 04-OCT-2000  
LOCUS A2463503  
DEFINITION 1M0272824F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0272824 F, genomic survey sequence.  
ACCESSION A2463503  
VERSION A2463503.1 GI:10621628  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0272 row: E column: 24  
Seq primer: CGTTGTAAACGACGCCAGT  
Classes: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/sex="Male"  
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/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 353  
A2463652/c 22 bp DNA linear GSS 04-OCT-2000  
LOCUS A2463652/c  
DEFINITION 1M0272812R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0272812 R, genomic survey sequence.  
ACCESSION A2463652  
VERSION A2463652.1 GI:10621777  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0272 row: E column: 12  
Seq primer: CACACAGAAACAGCTATGACC  
Classes: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES  
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/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 354  
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LOCUS 1M037415R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0374015 R, genomic survey sequence.  
ACCESSION AZ582403  
VERSION AZ582403.1 GI:11701249  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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JOURNAL Unpublished (2000)  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0374 row: J column: 15  
Seq primer: CACACGAAACACGATATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

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/clone\_1lb="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5414  
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Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 355  
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DEFINITION clone UGCGM0430A13 F, genomic survey sequence.  
ACCESSION AZ607658  
VERSION AZ607658.1 GI:11729848  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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JOURNAL Unpublished (2000)  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0430 row: A column: 13  
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Class: plasmid ends  
High quality sequence stop: 22.

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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAACAGAAAAA 5414  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 356  
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DEFINITION 1M0529D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ654691  
VERSION AZ654691.1 GI:11791837  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
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COMMENT Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: D column: 05  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
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/note="Vector: PMD42nv; Purified genomic DNA from M.  
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0.005 inch orifice at constant velocity. The sheared DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAACAGAAAAA 5414  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 357  
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DEFINITION 1M0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ760533  
VERSION AZ760533.1 GI:12868477  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0554 row: A column: 24  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0554A24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414  
DB 1 AAAAAAAAAAAAAAAAAA 22

RESULT 358  
A2779844/c 22 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0016112R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG2M0016112 R, genomic survey sequence.  
ACCESSION A2779844  
VERSION A2779844.1 GI:12910910  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
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Contact: Robert B. Weis  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0016 row: 1 column: 12  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414  
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 359  
A2785019 22 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0028E04R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG2M0028E04 R, genomic survey sequence.  
ACCESSION A2785019  
VERSION A2785019.1 GI:12921341  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0028 row: 8 column: 04  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAGAAAAA 5414  
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 360  
A2787098/c 22 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0033A05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG2M0033A05 F, genomic survey sequence.

ACCESSION  
A2787098  
VERSION  
A2787098.1 GI:12925520

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0033 row: A column: 05  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAGAAAAA 5414  
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 361  
A2787606/c 22 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0034G12P Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
clone UGCG2M0034G12 F, genomic survey sequence.

ACCESSION  
A2787606  
VERSION  
A2787606.1 GI:12925655

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: G column: 12  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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electrophoresis. Vector DNA was prepared from a derivative  
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inducible derivative of plasmid R1. The vector was ligated



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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 362  
AZ792704/c 22 bp DNA 1linear GSS 16-FEB-2001  
LOCUS 2M0045A24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
DEFINITION clone UGCG2M0045A24 F, genomic survey sequence.  
ACCESSION AZ792704  
VERSION AZ792704.1 GI:12936911  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
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Unpublished (2000)  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: A column: 24  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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electrophoresis. Vector DNA was prepared from a derivative  
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Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 363  
AZ810674/c 22 bp DNA 1linear GSS 20-FEB-2001  
LOCUS 2M0076B19P Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
DEFINITION clone UGCG2M0076B19 F, genomic survey sequence.  
ACCESSION AZ810674  
VERSION AZ810674.1 GI:12978158  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
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Niederhausern, A. and Wright, D., Weis, R.  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: B column: 19  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

FEATURES  
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/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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adapted DNA was purified and size-selected for a 9.5 to  
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of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 1

# RESULT 364

AZ820439 22 bp DNA linear GSS 20-FEB-2001  
LOCUS AZ820439/c

DEFINITION 2M0092K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0092K13 R, genomic survey sequence.

ACCESSION AZ820439

VERSION AZ820439.1 GI:12990443

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

Niederhausern,A. and Wright,D.,Weiss,R.  
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plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

COMMENT

JOURNAL

TITLE

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plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: K column: 13

Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0092K13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
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Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 1

# RESULT 365

AZ841661 22 bp DNA linear GSS 20-FEB-2001  
LOCUS AZ841661

DEFINITION 2M0139118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0139118 R, genomic survey sequence.

ACCESSION AZ841661

VERSION AZ841661.1 GI:13011569

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

COMMENT

JOURNAL

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: I column: 18

Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0139118"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 22

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

#### RESULT 366

AZ843514/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

22 bp DNA linear GSS 20-FEB-2001  
2M0142124F Mouse 10kb plasmid UUGCM library Mus musculus genomic  
clone UUGCM0142124 F, genomic survey sequence.  
AZ843514  
AZ843514  
GI:13013422  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contract: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0142 row: 1 column: 24  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

#### FEATURES

source

1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCM0142124"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGCM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 1

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

#### RESULT 367

AZ946102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

22 bp DNA linear GSS 27-APR-2001  
2M0207013R Mouse 10kb plasmid UUGCM library Mus musculus genomic  
clone UUGCM0207013 R, genomic survey sequence.  
AZ946102  
AZ946102  
GI:13812911  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contract: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0207 row: D column: 13  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

#### FEATURES

source

1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCM0207013"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGCM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."



/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="35c12"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 371

7A380A07P

LOCUS 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 380A07, forward sequence,  
genomic survey sequence.  
ACCESSION AL497713  
VERSION AL497713.1 GI:11873435  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 22)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.B., Rajandream, M.A. and Barrell, B.G.  
Direct Submision

TITLE  
JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
mlhesanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1..22  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="380A07"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

## RESULT 372

AG194579

LOCUS 22 bp DNA linear GSS 06-MAR-2004  
DEFINITION Pan troglodytes DNA, clone: RP43-072N05.TU, genomic survey  
sequence.  
ACCESSION AG194579  
VERSION AG194579.1 GI:45226755  
KEYWORDS GSS.  
SOURCE Pan troglodytes (Chimpanzee)  
ORGANISM Pan troglodytes

AG194579  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

1. Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of library RP-43  
Unpublished

## REFERENCE

2 (bases 1 to 22)  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
Direct Submision

## JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);  
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea  
(E-mail: redstone@mail.krrib.re.kr URL: <http://pds.grc.krrib.re.kr/>,  
Tel:82-42-866-7181, Fax:82-42-860-4409)  
Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the RAD process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.

## FEATURES

source

1..22  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-072N05.TU"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.3%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

## RESULT 373

AL038397

LOCUS 23 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566N082\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone  
DKFZP566N082, mRNA sequence.  
ACCESSION AL038397  
VERSION AL038397.1 GI:49682109  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## SOURCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 23)  
Ostenweider, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.

REFERENCE  
EST (Ostenweider, et al.)  
Unpublished (1999)

COMMENT  
Contact: MIPS

## FEATURES

source

1..23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566N082"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"

/clone\_1ib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421  
|||||  
2 TACAAAAAGAAAAATGAAAA 23

RESULT 374  
AL038592 23 bp mRNA linear EST 06-JUL-2004  
LOCUS  
DEFINITION DKFZP566G1446.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038592  
VERSION AL038592.1 GI:49682166  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 23)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

FEATURES  
source Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.  
location/Qualifiers  
1..23

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566G1446"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1ib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421  
|||||  
2 TACAAAAAGAAAAATGAAAA 23

RESULT 375  
AL038609 23 bp mRNA linear EST 06-JUL-2004  
LOCUS  
DEFINITION DKFZP566G0946.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038609  
VERSION AL038609.1 GI:49682169  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 23)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.

FEATURES  
source location/Qualifiers  
1..23

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566G0946"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1ib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421  
|||||  
2 TACAAAAAGAAAAATGAAAA 23

RESULT 376  
AL038688 23 bp mRNA linear EST 06-JUL-2004  
LOCUS  
DEFINITION DKFZP566J0646.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038688  
VERSION AL038688.1 GI:49682188  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 23)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

FEATURES  
source Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.  
location/Qualifiers  
1..23

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566J0646"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1ib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421  
|||||  
2 TACAAAAAGAAAAATGAAAA 23

RESULT 377  
CF300172/c 23 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION CF300172 7LEAF--04-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japónica cultivar-group) cDNA clone 7LEAF--04-H15, mRNA  
sequence.  
ACCESSION CF300172  
VERSION CF300172.1 GI:33671933  
KEYWORDS EST.

SOURCE Oryza sativa (japónica cultivar-group)  
ORGANISM

Oryza sativa (japónica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

# REFERENCE

1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source  
1..23  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39847"  
/clone="7LEAF-04-R15"  
/issue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice leaf Plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5386 AAGAAATTAATAAATACAAAA 5407  
|||  
22 AATTAATTAATAAATAAAAAA 1

RESULT 378 23 bp mRNA linear EST 18-AUG-2003  
CF332379 NACL--08-N21.q1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-N21, mRNA  
sequence.

ACCESSION CF332379 GI:33812983  
VERSION CF332379  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source  
1..23  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39847"  
/clone="NACL--08-N21"  
/issue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5392 TAAAAAATACAAAAAGAAA 5413  
|||  
22 TAAAAAATACAAAAAGAAA 1

RESULT 379 23 bp DNA linear GSS 03-OCT-2000  
A2425710  
LOCUS 1M0205123R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
DEFINITION clone UGCLM0205123 R, genomic survey sequence.

ACCESSION A2425710 GI:10549723  
VERSION A2425710  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0203 Row: L Column: 23  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence scop: 23.

# FEATURES

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/db\_xref="taxon:10090"  
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/clone\_1lb="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF159072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAA 5414  
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Db 2 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 380  
AZ447220 23 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0244E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0244E15 F, genomic survey sequence.  
ACCESSION AZ447220  
VERSION AZ447220.1 GI:10598989  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: B column: 15  
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Class: Plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAAAAGAAAA 5415  
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Db 1 AAAAAAAAAATTAATAAAAAAAAA 22

RESULT 381  
AZ801003 23 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0059J16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0059J16 F, genomic survey sequence.  
ACCESSION AZ801003  
VERSION AZ801003.1 GI:12953326  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0059 row: J column: 16  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: Plasmid ends  
High quality sequence stop: 23.  
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/mol\_type="genomic DNA"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to



adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATTCAGAAAAA 5413  
|||||  
DB 2 TAAAAAATTCAGAAAAA 23

RESULT 382  
LOCUS AZ973926 23 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0248N15F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
ACCESSION AZ973926  
VERSION AZ973926.1 GI:13845153  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Iselm, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0248 row: N column: 15  
Seq primer: CGTTCGTAACACACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 23.  
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/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|Jd|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1183 GAAGAGAGAGAGAGAAATCAG 1204  
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DB 23 GAAGAGAGAGAGAGAGACAG 2

RESULT 383  
LOCUS TA55C06P 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. Brucei sheared genomic DNA clone 55c06, forward sequence.  
ACCESSION AL455778  
VERSION AL455778.1 GI:11856729  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
1 (bases 1 to 23)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
Direct Subdivision  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4 GUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

source  
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/organism="Trypanosoma brucei"  
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Query Match 0.3%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATTCAGAAAAA 5414  
|||||  
DB 2 AAAAAAATTCAGAAAAA 23

RESULT 384  
LOCUS CA853764 24 bp mRNA linear EST 01-AUG-2003  
DEFINITION B12A03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone  
ACCESSION CA853764  
VERSION CA853764.1 GI:33390569  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 24)  
 AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.  
 TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Alkharouf, N.W.  
 Soybean Genomics and Improvement Laboratory (SGIL)  
 US Department of Agriculture (USDA), ARS, PSI  
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
 USA  
 Tel: 301 504 5750  
 Fax: 301 504 5728  
 Email: alkharouf@ars.usda.gov.

FEATURES  
 source location/Qualifiers  
 1..24

Query Match 0.3%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 2.3e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5414  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 385  
 CF312319/c 24 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--07-P12.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
 ABF--07-P12, mRNA sequence.  
 ACCESSION CF312319  
 VERSION CF312319.1 GI:33684080  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Euphorbiaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 24)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm, B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of BioScience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source location/Qualifiers  
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 /mol\_type="mRNA"  
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/tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
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 /note="Vector: pCR4-TOPO, Site 1: EcoRI, Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABF-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.3%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 2.3e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5414  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 386  
 A2781101/c 24 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0019J01P Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0019J01 F, genomic survey sequence.  
 ACCESSION A2781101  
 VERSION A2781101.1 GI:12913455  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0019 row: J column: 01  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.

FEATURES  
 source location/Qualifiers  
 1..24

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0019J01"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2282 GTCCAGATGACCTCAGAGCA 2303  
DB 24 GACCAATATGACCCAGAGCA 3

RESULT 387  
LOCUS AZ812579 24 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0079A23F Mouse 10kb plasmid UUGCM library Mus musculus genomic  
ACCESSION AZ812579  
VERSION AZ812579.1 GI:12981965  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0079 row: A column: 23  
Seq primer: CCGTGTAAACGACGCGCACT  
Clase: Plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1. 24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGCM0079A23"  
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/note="Vector: PMD23rv. Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAA 5414  
DB 3 AAAAAAAAAAAAAAAAAAAAA 24

RESULT 388  
LOCUS CF296213/c 21 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA  
sequence.  
ACCESSION CF296213  
VERSION CF296213.1 GI:33665246  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 21)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.T., Kim, J.K., Kim, Y.-K. and Nam, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
JOURNAL Contact: Nahm B.H.  
COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1. 21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="30DGS--06-H19"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E. coli DH10B"  
/note="Vector: PCR-TOP0. Site 1: BcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAA 5412  
DB 20 AAAAAAAAACAAAAAAAAAAAAA 1

RESULT 389  
LOCUS AL587602/c 23 bp mRNA linear EST 02-MAR-2001  
DEFINITION AL587602 BP Chicken Brain library Gallus gallus cDNA clone  
ROS059F08, mRNA sequence.

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ACCESSION      AL587602
VERSION        AL587602.1  GI:13192636
KEYWORDS       EST.
SOURCE         Gallus gallus (chicken)
ORGANISM       Gallus gallus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                Phasianidae; Gallus.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Murray, P.
TITLE          BP Chicken Brain Library
JOURNAL        Unpublished (2001)
COMMENT        Contact: Frazer Murray
                Dept. Genomics and Bioinformatics
                Roslin Institute
                Roslin, Midlothian, EH25 9PS, UK
                Tel: +44 (0)131 527 4200
                Fax: +44 (0)131 440 0434
                Email: frazer.murray@bbsrc.ac.uk
                GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
                (*6854-
                Seq primer: M13P.
FEATURES       Location/Qualifiers
                1..23
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /db_xref="taxon:9031"
                /clone="ROS059F08"
                /tissue_type="Brain"
                /dev_stage="Unknown"
                /lab_host="DH10B"
                /clone_lib="BP Chicken Brain Library"
                /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
                unidirectionally. Primer: Oligo dT, 5' adaptor sequence:
                5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
                Clontech (*6854-1)"
Query Match   0.3%; Score 16.8; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy           5393 AAAAAAATTCAAAAAGAGAAA 5413
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              23 AAAAAAAAAAAAAAAAAAGAGAA 3

RESULT 390
CF297907      23 bp      mRNA      linear      EST 15-AUG-2003
LOCUS         7LEAF--01-B05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B05, mRNA
sequence.
ACCESSION     CF297907
VERSION       CF297907.1  GI:33669668
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
                Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

```

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FEATURES       Location/Qualifiers
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                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /tissue_type="leaf"
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                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                was reverse transcribed and then used for PCR. mRNA was
                prepared from Arabidopsis thaliana overexpression line."
Query Match   0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy           5393 AAAAAAATTCAAAAAGAGAAA 5415
              ||||| ||||| ||||| |||||
              23 AAAAAAAAAAAAAAAAAAGAGAA 1

RESULT 391
CF334077      23 bp      mRNA      linear      EST 18-AUG-2003
LOCUS         JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION    library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                JMT--03-D17, mRNA sequence.
ACCESSION     CF334077
VERSION       CF334077.1  GI:33816466
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
                Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES       Location/Qualifiers
                1..23
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="JMT--03-D17"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                cDNA library (JMT)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                was reverse transcribed and then used for PCR. mRNA was
                prepared from Arabidopsis thaliana overexpression line."
Query Match   0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy           5393 AAAAAAATTCAAAAAGAGAAA 5415
              ||||| ||||| ||||| |||||

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RESULT 394  
 AZ645254/C  
 LOCUS  
 DEFINITION 23 bp DNA 1linear GSS 14-DEC-2000  
 1M0510005R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0510005 R, genomic survey sequence.  
 ACCESSION  
 AZ645254  
 VERSION  
 AZ645254.1 GI:11774572  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0510 row: O column: 05  
 Seq primer: CACACGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0510005"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.6; DB 1; Length 23;  
 Best Local Similarity 82.6%; Pred. No. 2.6e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAAA 5415  
 ||||| ||||| ||||| |||||  
 DB 23 AAAAAAAAAAAGAAAAAAA 1

RESULT 395  
 AZ970753/C  
 LOCUS  
 DEFINITION 23 bp DNA 1linear GSS 27-APR-2001  
 2M0244E01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0244E01 F, genomic survey sequence.  
 ACCESSION  
 AZ970753  
 VERSION  
 AZ970753.1 GI:13841980  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0244 row: B column: 01  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
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 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.6; DB 1; Length 23;  
 Best Local Similarity 82.6%; Pred. No. 2.6e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 841 TCTCCAGCAACCACTCCAC 863  
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 DB 23 TCACTCCCACTCCACCTCCAC 1

CL693171 23 bp DNA 1linear GSS 10-JUL-2004  
 LOCUS CL693171  
 DEFINITION PRI0160b\_B06.2 - PRI0160b.BR (33) Note: Recurring String Mixed  
 stage fosmid library of P. pacificus var. California Pristionchus  
 pacificus genomic, genomic survey sequence.  
 ACCESSION CL693171  
 VERSION CL693171.1 GI:50215079  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 23)  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 ApDB: an AcDB database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 CONTACT: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.  
 FEATURES  
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 /organism="Pristionchus pacificus"  
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 /db\_xref="taxon:54126"  
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 var. California"  
 /note="Vector: pBf108-5 Fosmid vector"

Query Match 0.3%; Score 16.6; DB 1; Length 23;  
 Best Local Similarity 82.6%; Pred. No. 2.6e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAGAA 5411  
 Db 1 AAAAAAAAAAACAATAAAAA 23

RESULT 397  
 AZ489586 19 bp DNA 1linear GSS 05-OCT-2000  
 LOCUS AZ489586  
 DEFINITION IM0322C12P Mouse 10kb plasmid UGCM1 library Mus musculus genomic  
 clone UGCM0322C12 F, genomic survey sequence.  
 ACCESSION AZ489586  
 VERSION AZ489586.1 GI:10659481  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0322 Row: C Column: 12  
 Seq primer: CGTGTAAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /db\_xref="taxon:10090"  
 /clone="UGCM0322C12"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UGCM1 library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (GI:473214|gb|AF19072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1181 GAGAAAGAGAGAGAGA 1198  
 Db 19 GAGAGAGAGAGAGAGA 2

RESULT 398  
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 LOCUS AZ983014/C  
 DEFINITION 2M0264H02P Mouse 10kb plasmid UGCM2 library Mus musculus genomic  
 clone UGCM0264H02 F, genomic survey sequence.  
 ACCESSION AZ983014  
 VERSION AZ983014.1 GI:13854241  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0264 row: H column: 02  
 Seq primer: CGTGTGAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

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 /strain="C57BL/6J"  
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 /clone\_lib="Mouse 10kb plasmid UUCG2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAG 1197

Db 19 AGAGAGAGAGAGAGAGAG 2

RESULT 399  
 AZ333204/c 23 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0062J11F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0062J11 F, genomic survey sequence.  
 ACCESSION AZ333204  
 VERSION AZ333204.1 GI:10397591  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

## Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 Plasmid inserts

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah

Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0062 row: J column: 11  
 Seq primer: CGTGTGAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 23.

## FEATURES

source

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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0062J11"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 23;  
 Best Local Similarity 94.4%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5258 CAGAGTAAAGTGAAGGA 5275

Db 21 CAGAGTGAAGTGAAGGA 4

RESULT 400  
 AJ658282 21 bp mRNA linear EST 28-JUN-2004  
 LOCUS AJ658282 KN277 Sus scrofa cDNA clone C0005212\_D02, mRNA sequence.  
 DEFINITION AJ658282  
 ACCESSION AJ658282  
 VERSION AJ658282.1 GI:49342351  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 1 (bases 1 to 21)  
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
 Development of cDNA and EST resources for studying reproduction and  
 embryo development in pigs and cattle

## Unpublished (2004)

Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.020425.c. Vector identified by cross-match with the -miniscore 20  
 and -mismatch 12 options. Vector:PBHScriptII(SK+) R. Site1: ECORI  
 R. Site2: NotI 5' Seg Primer M13P Normalised library constructed  
 from pooled early embryos, from 8-cell stage to blastocysts.  
 Clones available from UK Centre for Functional Genomics in Farm  
 Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
 www.airgenomics.org.

Location/Qualifiers



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source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005212_D02"
/issue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 401
AL048777 21 bp mRNA linear EST 28-JUN-2004
DEFINITION
AJ666203 CSEGRAN09 Sus scrofa cDNA clone C0000033_C15, mRNA
sequence.
ACCESSION
AJ666203 GI:49350654
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 21)
Anderson, S.I., Philayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arts.genomics.org.
Location/Qualifiers
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C15"
/issue_type="placenta"
/clone_lib="CSEGRAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

FEATURES
source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C15"
/issue_type="placenta"
/clone_lib="CSEGRAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 402
AL048777 21 bp mRNA linear EST 04-SEP-2003
LOCUS

```

```

DEFINITION
DKFZp566N053.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566N053, mRNA sequence.
ACCESSION
AL048777 GI:4727848
VERSION
AL048777.1 GI:4727848
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuenberg, Germany.
Location/Qualifiers
1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N053"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 403
CP282216 21 bp mRNA linear EST 14-AUG-2003
LOCUS
CP282216
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K01,
mRNA sequence.
ACCESSION
CP282216 GI:33659603
VERSION
CP282216
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacoidae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="14ETL--09-K01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

FEATURES
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1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="14ETL--09-K01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

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/clone\_11b="Rice etiolated leaf plasmid cDNA library (14EST)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413  
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

RESULT 404  
LOCUS CF292703/c 21 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--01-K01.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--01-K01, mRNA sequence.

ACCESSION CF292703  
VERSION CF292703  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 21)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/db\_xref="taxon:39947"  
/clone="30DGS--01-K01"  
/issue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_11b="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 405  
LOCUS CF295642/c 21 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K20, mRNA sequence.

ACCESSION CF295642  
VERSION CF295642  
GI:33664675

KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 21)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/clone="30DGS--05-K20"  
/issue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_11b="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 406  
LOCUS CF297615

DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION CF297615  
VERSION CF297615  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 21)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"

/db\_xref="taxon:39947"  
/clone="30DGS--08-J10"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_11b="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413  
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 407  
CF298322/c 21 bp mRNA linear EST 15-AUG-2003  
LOCUS CF298322/c 71EAF--01-K14.b1 Rice leaf plasmid cDNA library II (71EAF) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 71EAF--01-K14, mRNA  
sequence.

ACCESSION CF298322 GI:33670083  
VERSION CF298322  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..21

/organism="Oryza sativa (japonica cultivar-group)"  
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/clone="71EAF--01-K14"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_11b="Rice leaf plasmid cDNA library II (71EAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413  
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 408  
CF300809/c 21 bp mRNA linear EST 15-AUG-2003  
LOCUS CF300809/c 71EAF--05-G20.b1 Rice leaf plasmid cDNA library II (71EAF) Oryza  
DEFINITION

ACCESSION CF300809.1 GI:33672570  
VERSION CF300809  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..21

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="71EAF--05-G20"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_11b="Rice leaf plasmid cDNA library II (71EAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413  
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 409  
CF312715 21 bp mRNA linear EST 15-AUG-2003  
LOCUS CF312715 ABF--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABF--08-J10, mRNA sequence.

ACCESSION CF312715 GI:33684476  
VERSION CF312715  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

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source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABP--08-J10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABP3-overexpressing transgenic rice plasmid
CDNA library (ABP)"
/note="vector: PCR4-TOPO, Site.1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 410
LOCUS CF316073 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-D16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-D16, mRNA sequence.
CF316073
ACCESSION CF316073.1 GI:33687834
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-D16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOPO, Site.1: EcoRI, Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 411
LOCUS CF326952 21 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-D20.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--01-D20, mRNA
sequence.
CF326952
ACCESSION CF326952.1 GI:33802159
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-D20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO, Site.1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 412
LOCUS CF327391 21 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-N18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--01-N18, mRNA
sequence.
CF327391
ACCESSION CF327391.1 GI:33803041
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

```

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
SOURCE location/Qualifiers

1. 21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="NACL-01-N18"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 413  
LOCUS CF332956/c 21 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--01-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--01-K14, mRNA sequence.  
ACCESSION CF332956  
VERSION CF332956.1 GI:33814150  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzaeae; Oryza.  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
SOURCE

1. 21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT--01-K14"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 414  
LOCUS CF338057 21 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--08-M03, mRNA sequence.  
ACCESSION CF338057  
VERSION CF338057.1 GI:33824485  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzaeae; Oryza.  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
SOURCE location/Qualifiers

1. 21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT--08-M03"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 415  
LOCUS CF338522/c 21 bp mRNA linear EST 18-AUG-2003  
DEFINITION RC14--01-P04.g1 Regenerated callus lambda phage cDNA library (RC14) Oryza sativa (japonica cultivar-group) cDNA clone RC14--01-P04, mRNA sequence.  
ACCESSION CF338522  
VERSION CF338522.1 GI:33825432  
KEYWORDS EST.

**SOURCE**  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

**REFERENCE**  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**FEATURES**  
source  
1..21  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39847"  
/clone="RCU1-01-P04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_idb="Regenerated callus lambda phage cDNA library (RCU1)"  
/note="Vector: pBluescript SK(+), Site\_1: SctI, Site\_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. XhoI was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

**Query Match**  
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 21;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 5393 AAAAAAAAAACAAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

**RESULT 416**  
CNS46489 21 bp mRNA linear EST 30-APR-2004  
LOCUS EST 18633 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
DEFINITION cDNA clone B3CS57RB007B11 3', mRNA sequence.  
ACCESSION CNS46489  
VERSION CNS46489.1 GI:46911114  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
1 (bases 1 to 21)  
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr

**FEATURES**  
Seq primer: T7.  
source  
1..21  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS57RB007B11"  
/dev\_stage="ripe stage"  
/clone\_idb="Ripe Grape Berry Lambda Triplex2 Library"  
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

**Query Match**  
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 21;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 5393 AAAAAAAAAACAAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

**RESULT 417**  
CNS46504 21 bp mRNA linear EST 30-APR-2004  
LOCUS EST 18648 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera  
DEFINITION cDNA clone B3CS57RB007G04 3', mRNA sequence.  
ACCESSION CNS46504  
VERSION CNS46504.1 GI:46911129  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
1 (bases 1 to 21)  
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
Unpublished (2002)  
Contact: Hamdi S.  
UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7.

**FEATURES**  
source  
1..21  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="B3CS57RB007G04"  
/dev\_stage="ripe stage"  
/clone\_idb="Ripe Grape Berry Lambda Triplex2 Library"  
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Oriented library"

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RESULT 418
LOCUS CN546595/c 21 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18739 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CN546595
VERSION CN546595.1 GI:46911220
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidae; Vitaceae; Vitis.
1 (bases 1 to 21)
Couture,C., Agasee,A., Ageorges,A., Atanasova,R., Barileu,F.,
Hamdi,S., Komleu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
source
1..21
location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008G02"
/dev_stage="ripe stage"
/clone_1fb="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"
Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAA 5413
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 419
LOCUS COT79794/c 21 bp mRNA linear EST 05-AUG-2004
DEFINITION BL007D B05 6-Day Axotol Tail Blastema (6DAXBL) Ambystoma mexicanum
cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION COT79794
VERSION COT79794.1 GI:50995774
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axotol)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomacidae;
Ambystoma.
1 (bases 1 to 21)
Habermann,B., Behn,A.G., Herklitz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schaeckert,H.K., Wiebe,G. and Tanaka,B.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
CDNA libraries
Genome Biol. (2004) in press
Contact: Eily M. Tanaka
Tanaka Lab

```

```

Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfeifenhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpl-cbg.de
Plate: BL007D row: 05 column: E
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
source
1..21
location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/clone_1fb="6-Day Axotol Tail Blastema (6DAXBL)"
/notes="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
Unnormalized cDNA plasmid library prepared by invitrogen.
Size fractionated mRNA was polyA+ primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-RNA. Average insert size is 1.67 kb.
TAG_L1B=6DAXBL"
Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAA 5413
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 420
LOCUS AZ317208/c 21 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0035102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035102 R, genomic survey sequence.
ACCESSION AZ317208
VERSION AZ317208.1 GI:10365804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
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1..21
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035102"
/sex="Male"

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5395 AAAAATACAAAGAAAAA 5415

Db 21 AAAAAAAAAAAAAAAAAAAAA 1

## RESULT 421

AZ348593

LOCUS 21 bp DNA linear GSS 29-SEP-2000

DEFINITION IM0085A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0085A13 F, genomic survey sequence.

ACCESSION

AZ348593

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0085 row: A column: 13

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0085A13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAA 5413

Db 1 AAAAAAAAAAAAAAAAAAAAA 1

## RESULT 422

AZ350611

LOCUS 21 bp DNA linear GSS 29-SEP-2000

DEFINITION IM0086C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0086C14 F, genomic survey sequence.

ACCESSION

AZ350611

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: C column: 14

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0086C14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"



/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 423  
AZ386711 21 bp DNA linear GSS 02-OCT-2000  
LOCUS  
DEFINITION 1M0145016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION  
AZ386711  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
MUS musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: 0 column: 16  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 424  
AZ386794 21 bp DNA linear GSS 02-OCT-2000  
LOCUS  
DEFINITION 1M0145022R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION  
AZ386794  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
MUS musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: 0 column: 22  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
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/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

## RESULT 425

AZ389287

LOCUS AZ389287 21 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0149A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0149A13 R, genomic survey sequence.

ACCESSION AZ389287  
VERSION AZ389287.1 GI:10502995

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0149 row: A column: 13  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source location/Qualifiers

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/lab\_host="E. Coli strain X110-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

## RESULT 426

AZ389687

LOCUS AZ389687 21 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150B10 R, genomic survey sequence.

ACCESSION AZ389687  
VERSION AZ389687.1 GI:10503395

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0150 row: B column: 10  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain X110-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5413  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 427  
AZ406936 21 bp DNA linear GSS 03-OCT-2000  
LOCUS IM0176E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0176E24 F, genomic survey sequence.  
ACCESSION AZ406936  
VERSION AZ406936.1 GI:10530949  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0176 row: B column: 24  
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Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0176E24"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428  
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LOCUS IM0186D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0186D23 F, genomic survey sequence.  
ACCESSION AZ412739  
VERSION AZ412739.1 GI:10536752  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0186 row: D column: 23  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAAAGAAAA 5413
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Db      21 AAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 429  
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LOCUS 1M0186N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0186N08 R, genomic survey sequence.

ACCESSION AZ412931 GI:10536944  
VERSION AZ412931.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B., R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0186 row: N column: 08  
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Class: plasmid ends

High quality sequence stop: 21.  
Location/Qualifiers  
1. 21

FEATURES  
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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAAAGAAAA 5413
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Db      21 AAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 430  
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LOCUS 1M0189M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0189M07 R, genomic survey sequence.

ACCESSION AZ415029 GI:10539042  
VERSION AZ415029.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B., R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0189 row: M column: 07  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends

High quality sequence stop: 21.  
Location/Qualifiers  
1. 21

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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAAA 5413  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 431  
AZ465890 21 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0276F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0276F07 F, genomic survey sequence.

ACCESSION AZ465890  
VERSION AZ465890.1 GI:10624015  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0276 row: F column: 07  
Seq primer: CCGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source Location/Qualifiers

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0276F07"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAAA 5413  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 432  
AZ611116 21 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0436N02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0436N02 R, genomic survey sequence.

ACCESSION AZ611116  
VERSION AZ611116.1 GI:11733306  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0436 row: N column: 02  
Seq primer: CACACAGGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source Location/Qualifiers

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0436N02"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 433  
AZ611423 21 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0437E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0437E13 R, genomic survey sequence.  
ACCESSION  
AZ611423  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0437 row: B column: 13  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

#### FEATURES

source

1. 21  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0437E13"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 434  
AZ615628 21 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0444M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0444M19 R, genomic survey sequence.  
ACCESSION  
AZ615628  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0444 row: M column: 19  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

#### FEATURES

source

1. 21  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0444M19"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 435  
AZ627843/c 21 bp DNA 1linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0474H03P Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
ACCESSION AZ627843  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

CONTACT: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 Row: H Column: 03  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

#### FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0474H03"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413  
|||||  
21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 436  
AZ627845 21 bp DNA 1linear GSS 13-DEC-2000  
LOCUS  
DEFINITION 1M0474G11P Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
ACCESSION AZ627845  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhuesern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

CONTACT: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 Row: G Column: 11  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

#### FEATURES

1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0474G11"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
Inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5413  
|||||  
Db 21 AAAAAAAAAAAAAAAAAA 1

## RESULT 437

A2657727

LOCUS 21 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0534B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0534B07 F, genomic survey sequence.

A2657727

ACCESSION A2657727.1 GI:11794873

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0534 row: B column: 07  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

JOURNAL

COMMENT

FEATURES

source

1. 21  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0534B07"  
/sex="Male"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 21

## RESULT 438

A2765552

LOCUS 21 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0564011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0564011 F, genomic survey sequence.

A2765552

ACCESSION A2765552.1 GI:12883741

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: O column: 11  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

JOURNAL

COMMENT

FEATURES

source

1. 21  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564011"  
/sex="Male"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 21

ACCESSION A2765552.1 GI:12883741

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: O column: 11  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

JOURNAL

COMMENT



adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

## RESULT 439

LOCUS A2769976 21 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0571111F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0571111 F, genomic survey sequence.

ACCESSION A2769976  
VERSION A2769976.1 GI:12890681

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0571 row: 1 column: 11  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

## FEATURES

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1. 21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0571111"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5413  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

## RESULT 440

LOCUS A2792613 21 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0045M12 F, genomic survey sequence.

ACCESSION A2792613  
VERSION A2792613.1 GI:12936725

## KEYWORDS

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: M column: 12  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

## FEATURES

## source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5401 ACACAAAGAAAAATGAAA 5421  
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21 ACACAAAGAAAAATGAAA 1

RESULT 441  
A2793486 21 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0046G18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
DEFINITION clone UGCG2M0046G18 R, genomic survey sequence.

ACCESSION A2793486 GI:12938487

VERSION A2793486.1 GI:12938487

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.

Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0046 row: G column: 18

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21  
/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG2M0046G18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCACAAAAAGAAA 5413  
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21 AAAAAATTCACAAAAAGAAA 1

RESULT 442

A2799327

21 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0056C09R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

DEFINITION clone UGCG2M0056C09 R, genomic survey sequence.

ACCESSION A2799327

VERSION A2799327.1 GI:12950331

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weis,R.

Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0056 row: C column: 09

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21  
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/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG2M0056C09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAAAAA 21

## RESULT 443

A2810054

LOCUS A2810054 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0074E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0074E19 F, genomic survey sequence.

ACCESSION A2810054

VERSION A2810054.1 GI:12976935

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: B column: 19

Seq primer: CGTGTAAACACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0074E19"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

0.3%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAAAAA 21

## RESULT 444

A2815424

LOCUS A2815424 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0083H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0083H1 R, genomic survey sequence.

ACCESSION A2815424

VERSION A2815424.1 GI:12985332

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0083 row: H column: 11

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0083H11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

0.3%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 445  
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 LOCUS 2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0089110 R, genomic survey sequence.  
 ACCESSION A2819181  
 VERSION A2819181  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT Robert B. Weiss  
 UNIVERSITY of Utah  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 TEL: 801 585 5606  
 FAX: 801 585 7177  
 EMAIL: ddunn@genetics.utah.edu  
 INSERT LENGTH: 10000 Std Error: 0.00  
 PLATE: 0089 row: 1 column: 10  
 SEQ PRIMER: CACACAGGAAACGCTATGACC  
 CLASS: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0089110"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413  
 ||||| ||||| ||||| |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 446  
 A2832198 21 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0112P20 F, genomic survey sequence.  
 ACCESSION A2832198  
 VERSION A2832198  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT Robert B. Weiss  
 UNIVERSITY of Utah  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 TEL: 801 585 5606  
 FAX: 801 585 7177  
 EMAIL: ddunn@genetics.utah.edu  
 INSERT LENGTH: 10000 Std Error: 0.00  
 PLATE: 0112 row: P column: 20  
 SEQ PRIMER: CGTGTAAACGACGCCAGT  
 CLASS: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0112P20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAA 5413  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 447  
 A2843603 21 bp DNA 1linear GSS 20-FEB-2001  
 LOCUS A2843603  
 DEFINITION 2M0142106R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 clone UGCGM0142106 R, genomic survey sequence.

ACCESSION A2843603  
 VERSION A2843603.1 GI:13013511  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Authors: Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0142 row: 1 column: 06  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends

FEATURES  
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 /db\_xref="taxon:10090"  
 /clone="UGCGM0142106"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAA 5413

Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 448  
 A2853429 21 bp DNA 1linear GSS 21-FEB-2001  
 LOCUS A2853429  
 DEFINITION 2M0156D09R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 clone UGCGM0156D09 R, genomic survey sequence.

ACCESSION A2853429  
 VERSION A2853429.1 GI:13041543  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Authors: Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0136 row: D column: 05  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends

FEATURES  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
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 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5395 AAAAAAAAAAGAAAA 5415  
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Db 1 AAAAAAAAAAACAAAAA 21

RESULT 449  
A2960063

LOCUS 21 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0228A01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0228A01 F, genomic survey sequence.

ACCESSION A2960063  
VERSION A2960063.1 GI:13831290

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
JOURNAL  
COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: A column: 01

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES  
source

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Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0228A01"

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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAA 21

RESULT 450

BH000837

LOCUS 21 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0288020R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0288020 R, genomic survey sequence.

ACCESSION BH000837  
VERSION BH000837.1 GI:13872063

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
JOURNAL  
COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: O column: 20

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES  
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Location/Qualifiers

/organism="Mus musculus"

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/clone="UUGC2M0288020"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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electrophoresis. Vector DNA was prepared from a derivative

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inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAA 21

RESULT 451  
CF282024/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF282024 22 bp mRNA linear EST 14-AUG-2003  
14ETL--09-F13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F13,  
mRNA sequence.  
CF282024  
CF282024.1 GI:33659411  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukariyocae; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongjin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1..22  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
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RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||  
22 AAAAAAAAAAAAAAAAAAAAAA 2

DB 22

RESULT 452  
CF298427/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF298427 22 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M24, mRNA  
sequence.  
CF298427  
CF298427.1 GI:33670188  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukariyocae; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University  
Yongjin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
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/organism="Oryza sativa (japonica cultivar-group)"  
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/db\_xref="taxon:39947"  
/clone="7LEAF--01-M24"  
/issue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAGAAAAA 5415  
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21 AAAAAAAAAAAAAAAAAAAAAA 1

DB 21

RESULT 453  
CF310486  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF310486 22 bp mRNA linear EST 15-AUG-2003  
ABF--05-C16.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABF--05-C16, mRNA sequence.  
CF310486  
CF310486.1 GI:33682247  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukariyocae; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 22)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongjin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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/organism="Oryza sativa (japonica cultivar-group)"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

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Query Match      0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 TTTAAAAATTCAGAAAAAGAAA 5411
Db      2 TTTAAAAATTCAGAAAAAGAAA 22

RESULT 454
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DEFINITION BL003B.H01 6-Day Axiolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
ACCESSION  CO778290
VERSION     CO778290.1 GI:50994270
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axiolotl)
ORGANISM    Ambystoma mexicanum
            Bufoyola; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Habermann,B., Behn,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Eppelstein,H.H., Schackert,H.K., Wiede,G., and Tanaka,E.M.
            An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
JOURNAL     Genome Biol. (2004) In press
COMMENT     Contract: Eily M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pflotenauerstrasse 108, 01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpl-cbg.de
            Plate: BL003B row: 01 column: H
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
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                /cissue_type="Tail Blastema"
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                /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
                Unnormalized cDNA plasmid library prepared by Invitrogen.
                Size fractionated mRNA was polyAT primed and cloned into
                NotI-SalI site of pCMVSPORT6. Bacterial host is
                EMDH10B-TONA. Average insert size is 1.67 kb.
                TAG_LIB=6DaxBL"

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REFERENCE
AUTHORS    Bufoyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
            1 (bases 1 to 22)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weise,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Published (2000)
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0005 row: K column: 17
            Seq primer: CGTGTAAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES
            source
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="M0005K17"
                /sex="Male"
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                /clone_lib="Mouse 10kb plasmid UUC1M library"
                /note="Vector: PMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

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Query Match      0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 TTTAAAAATTCAGAAAAAGAAA 5413
Db      1 TTTAAAAATTCAGAAAAAGAAA 21

RESULT 455
LOCUS      AZ304806      22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION 1M0005K17F Mouse 10kb plasmid UUC1M library Mus musculus genomic
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ACCESSION  AZ304806
VERSION     AZ304806.1 GI:10341191
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus

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Query Match      0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 TTTAAAAATTCAGAAAAAGAAA 5413
Db      2 TTTAAAAATTCAGAAAAAGAAA 22

RESULT 456
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DEFINITION 1M0127H16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUC1M0127H16 F, genomic survey sequence.
ACCESSION  AZ374487
VERSION     AZ374487.1 GI:10488187
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Bufoyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



REFERENCE  
AUTHORS

1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0127 row: H column: 16  
Seq primer: CGTGTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

## source

1. 22  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0127H16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAATCAAAAAAGAAA 5413  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

## RESULT 457

AZ505769  
LOCUS 22 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0346A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0346A10 R, genomic survey sequence.  
ACCESSION AZ505769  
VERSION AZ505769.1 GI:10687085  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0346 row: A column: 10  
Seq primer: CACACGGAACGCGTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

## source

1. 22  
Location/Qualifiers

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0346A10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAATCAAAAAAGAAA 5413  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

## RESULT 458

AZ823875  
LOCUS 22 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0098K07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0098K07 F, genomic survey sequence.  
ACCESSION AZ823875  
VERSION AZ823875.1 GI:12993795  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)

**AUTHORS**  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0098 row: K column: 07  
Seq primer: CGTTGTAAAACACACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

**FEATURES**  
source  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0098K07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 22;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**  
5393 AAAAAAAAAAAGAAAA 5413  
|||||  
1 AAAAAAAAAAAAAAAAAA 21

**RESULT 459**  
AA845735 22 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION  
2M014507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M014507 R, genomic survey sequence.  
ACCESSION  
AA845735 1 GI:113015643  
VERSION  
AA845735.1  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
REFERENCE  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

**TITLE**  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: J column: 07  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

**FEATURES**  
source  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0145J07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 22;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**  
5395 AAAAAAAAAAAGAAAA 5415  
|||||  
22 AAAAAAAAAAAAAAAAAA 2

**RESULT 460**  
TA303605P 22 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION  
T. brucei sheared genomic DNA clone 303605, forward sequence.  
ACCESSION  
TA303605 1 GI:11865504  
VERSION  
TA303605.1  
KEYWORDS  
GSS.  
SOURCE  
Trypanosoma brucei  
Trypanosoma brucei  
Bukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 22)  
REFERENCE  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Omond,D., Harris,B., El-Sayed,N., Hou,L.,

TITLE Melville, S.B., Rajandream, M.A. and Barrell, B.G.  
JOURNAL Direct Submission

## COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nh@sanger.ac.uk  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

## source

1..22  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="303g05"

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## OR

5405 AAAAGAAAAATGAAATATAA 5425  
1 AAAAAAAAAAAGAAAAAAA 21

## DB

RESULT 461  
LOCUS CL693160 22 bp DNA linear GSS 10-JUL-2004  
DEFINITION PRI0160a\_P09.2 - PRI0160a.BR (32) Note: Recurring String Mixed  
stage fosmid library of P. pacificus var. California Pristionchus  
pacificus genomic, genomic survey sequence.  
CL693160  
VERSION CL693160.1 GI:50215068  
KEYWORDS GSS.

SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 22)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
ApDB: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL Contact: Sommer RJ  
Evolunary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39 Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498

## COMMENT

Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

## FEATURES

## source

1..22  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBplfos-5 fosmid vector"

Query Match 0.3%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## OR

5395 AAAAATACAAAAAGAAAAA 5415  
1 AAAAAAAAAAAGAAAAAAA 21

## DB

RESULT 462  
LOCUS AL048776 23 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZ0566N213\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone  
DKFZ0566N213, mRNA sequence.  
AL048776  
VERSION AL048776.1 GI:4727847  
KEYWORDS EST.

SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 23)  
Koehler, K., Beyer, A., Mewes, H.W., Gaassenhuber, J. and Wiemann, S.  
EST (Koehler, et al.)  
Unpublished (1999)  
Contact: MIPS

## COMMENT

## FEATURES

## source

1..23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZ0566N213"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_lib="566 (synonym: hfkd2)"  
/note="Vector: pMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## OR

5392 TAAAAAATACAAAAAGAAA 5412  
3 TAAAAAAGAAAAAAGAAAAA 23

## DB

RESULT 463  
LOCUS AL587621 23 bp mRNA linear EST 02-MAR-2001  
DEFINITION AL587621 BP Chicken Brain Library Gallus gallus cDNA clone  
ROS059H07, mRNA sequence.  
AL587621  
VERSION AL587621.1 GI:13192655  
KEYWORDS EST.

SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 23)

## REFERENCE

Murray, F.  
BP Chicken Brain Library  
Unpublished (2001)  
Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434

## COMMENT

Email: frazer.murray@berc.ac.uk  
 GCGGCCCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech  
 (\*6854-

FEATURES  
 source  
 Seq primer: M13P.  
 Location/Qualifiers  
 1..23

/organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="R05059H07"  
 /tissue\_type="brain"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B"  
 /clone\_1ib="BP Chicken Brain Library"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3', 3' adaptor sequence: 5' GCGGCCCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (\*6854-1)"

Query Match  
 Best Local Similarity 81.8%; Pred. No. 2.8e+02; Length 23;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAAT 5416  
 Db 23 AAAAAAAAAAAAAAAAAAAAAAT 2

RESULT 464  
 BQ590647/c 23 bp mRNA linear EST 06-DEC-2002  
 LOCUS S015086-024-018-P17-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 DEFINITION cDNA clone 024-018-P17 5-PRIME, mRNA sequence.  
 ACCESSION BQ590647  
 VERSION BQ590647.1 GI:26120230  
 KEYWORDS EST.

SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 23)  
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,  
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, D., Lehrach, H.  
 and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp1z-koeln.mpg.de  
 Insert length: 23 Std Error: 0.00  
 Plate: 18 row: P column: 17  
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.  
 Location/Qualifiers  
 1..23

FEATURES  
 source

/organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:189468"  
 /db\_xref="taxon:161934"  
 /clone="024-018-P17"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_1ib="MP1Z-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI;

cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primary sites and  
 orientation:  
 SP6-SalI-CCACGGGTCCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 Project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match  
 Best Local Similarity 85.7%; Pred. No. 2.8e+02; Length 23;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5394 AAAAAATACAAAAAGAAAAA 5414  
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 465  
 BX559898/c 23 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX559898 Glossina morsitans morsitans adult infected gut Glossina  
 DEFINITION morsitans morsitans cDNA clone Tse46d05\_p1c, mRNA sequence.  
 ACCESSION BX559898  
 VERSION BX559898.1 GI:33367802  
 KEYWORDS EST.

SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 23)  
 Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonald, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 14519198  
 PUBMED 12281942

COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.  
 Location/Qualifiers  
 1..23

/organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse46d05\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_1ib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match  
 Best Local Similarity 85.7%; Pred. No. 2.8e+02; Length 23;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5401 ACAAAGAGAAAAATGAAA 5421  
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 466  
LOCUS CF279593/c 23 bp mRNA 1linear EST 14-AUG-2003  
DEFINITION 14ETL--05-P06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-P06,  
mRNA sequence.  
ACCESSION CF279593  
VERSION CF279593.1 GI:33656979  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
Eriocaulaceae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Naim B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1..23  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ETL--05-P06"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="R.coli DH10B"  
/clone\_11b="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOPO, Site 1: SCOR1; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5405 AAAAGAAAAATGAAATATA 5425  
|||||  
Db 22 AAAAGAAAAATGAAATATA 5425

RESULT 467  
LOCUS AZ621676 23 bp DNA 1linear GSS 13-DEC-2000  
DEFINITION 1M0455007F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0455007 F, genomic survey sequence.  
ACCESSION AZ621676  
VERSION AZ621676.1 GI:11743962  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0455 row: J column: 07  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0455007"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g1473214|gb|AF19072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5396 AAAATACAAAAAAGAAAAAT 5416  
|||||  
Db 1 AAAATACAAAAAAGAAAAAT 5416

RESULT 468  
LOCUS AZ817623 23 bp DNA 1linear GSS 20-FEB-2001  
DEFINITION 2M0087N09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0087N09 F, genomic survey sequence.  
ACCESSION AZ817623  
VERSION AZ817623.1 GI:12987531  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,  
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0087 row: N column: 09  
Seq primer: CGTTGTTAAACGACGCGCCAGT  
Class: plasmid ends  
high quality sequence stop: 23.

Query Match	0.3%	Score 16.2;	DB 1;	Length 23;
Best Local Similarity	85.7%	Pred. No. 2.8e+02;		
Matches 18;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

RESULT	469				
A1371092/c					
LOCUS					
DEFINITION	A1371092	19 bp	mRNA	linear	EST 16-FEB-1999
	tao7g09.41	NCI CGAP Brn3	Homo sapiens	cDNA clone IMAGE:2043424	3'
	similar to TR:Q26195	Q26195	PVAL GENE.	contains L1.b3	L1
	repetitive element ;,	mRNA sequence.			

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
1 (bases 1 to 19) NCI/NINDS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BIGAP), Tumor Gene Index Unpublished (1998)	Contact: Robert Stransberg, Ph.D. Email: <a href="mailto:CGAPdb-remail@nih.gov">CGAPdb-remail.nih.gov</a> Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www-bio.1lnl.gov/bdnp/image/image.html](http://www-bio.1lnl.gov/bdnp/image/image.html)

Trace considered overall poor quality  
Insert Length: 536 Std Error: 0.00  
Seq primer: -40UP from G13co  
High quality sequence stop: 1.

Query Match	0.34;	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.54;	Pred. No. 2.6e+02;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

RESULT 470	LOCUS	DEFINITION
A2654747/c	A2654747	19 bp DNA linear GSS 14-DEC-2000
	IN0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic	
	clone UUGC1M0529F08 F, genomic survey sequence.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 19)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellam,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausem,A. and Wright,D. Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000	Std Error: 0.00		
	Plate: 0529	row: F	column: 08	
	Seq primer: CGTTGTAAACGACGCGCCACT			
	Class: plasmid ends			

High quality sequence stop: 19.  
Location/Qualifiers

1.19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGCM0529F08"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGGCM library"  
/note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent R. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAAATGAAA 5421  
19 AAAAAAAAAAAAAAAAAA 1

RESULT 471  
CL693177 19 bp DNA linear GSS 10-JUL-2004  
LOCUS PRI0160b\_G03 - PRI0160b.BR (19) Note: Recurring String Mixed  
DEFINITION Bage fosmid library of P. pacificus var. California Pristionchus  
ACCESSION CL693177  
VERSION CL693177.1 GI:50215085  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 19)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
ApplDB: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Classes: fosmid ends.  
Location/Qualifiers  
1.19  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"

/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBplfos-5 Fosmid vector"

Query Match 0.3%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5395 AAAAAATCAAAAAAGAAA 5413  
1 AAAAAAAAAAAAAAAAAA 19

RESULT 472  
A2375620 20 bp DNA linear GSS 02-OCT-2000  
LOCUS IM0129A08F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
DEFINITION clone UGGCM0129A08 F, genomic survey sequence.  
ACCESSION A2375620  
VERSION A2375620.1 GI:10489320  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Place: 0129 row: A column: 08  
Seq primer: CGTTGTAAACGACGCGCAGT  
Classes: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1.20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGGCM0129A08"  
/sex="Male"  
/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGGCM library"  
/note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5393 AAAAAAAAAACAAAAAGAA 5411  
|||||  
2 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 473  
AZ949997  
LOCUS 20 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0213J24R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
ACCESSION AZ949997  
VERSION AZ949997.1 GI:13821224  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0213 row: D column: 24  
Seq primer: CACACAGAAACGATGACG  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0213D24"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5393 AAAAAAAAAACAAAAAGAA 5411  
|||||  
2 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 474  
AZ345540/C  
LOCUS 21 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0080P05F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
ACCESSION AZ345540  
VERSION AZ345540.1 GI:10424777  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: P column: 05  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG1M0080P05"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."





REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0028 row: I column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M028121"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 196 TGCCCAACCCCATCTCCGTC 217  
|||  
Db 22 TGTCACACCCCATCACCAACC 1

RESULT 478  
BH000233 22 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0287121R Mouse 10kb plasmid UUC2M library Mus musculus genomic clone UUC2M0287121 R, genomic survey sequence.  
ACCESSION BH000233  
VERSION BH000233.1 GI:13871459  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0287 row: L column: 21  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M0287121"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGA 5410  
|||  
Db 1 AAAAAAAAAAAAAAAAAAGA 22

RESULT 479  
BG668047 18 bp mRNA linear EST 30-APR-2001  
LOCUS DRABUA12 Rat DRG library Rattus norvegicus cDNA clone DRABUA12 5', mRNA sequence.  
DEFINITION BG668047  
ACCESSION BG668047  
VERSION BG668047.1 GI:13889969  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 18)

**AUTHORS** Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C., Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang, X., Chen, Z., Han, Z.G. and Zhang X.

**TITLE** Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain

**JOURNAL MEDLINE** 22056133

**PUBMED** 12060780

**COMMENT** Contact: Zhang Xu  
Laboratory of Sensory System  
Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China  
Tel: 86-21-64748700-121  
Fax: 86-21-64713446  
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chc.sh.cn)

**PCR PRIMERs**

**FORWARD:** T3  
**BACKWARD:** T7  
**Seq primer:** T3  
**POLYA=No.**

**FEATURES**

**source** 1. 18  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="DRABUA12"  
/sex="male"  
/issue\_type="dorsal root ganglion"  
/dev\_stage="adult"  
/clone\_1ib="Rat DRG library"

**Query Match** 0.3%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1178 TCAGAGAAAGAGAGAGA 1194  
|||  
17 TCAGAGAGAGAGAGAGA 1

**DB** 17 TCAGAGAGAGAGAGAGA 1

**RESULT 480**

**LOCUS** BQ594437 18 bp mRNA linear EST 06-DEC-2002

**DEFINITION** E012442-024-M20-SP6 MP12-ADIS-024-developing root Beta vulgaris

**ACCESSION** BQ594437

**VERSION** BQ594437.1 GI:26124020

**KEYWORDS** EST.

**SOURCE** Beta vulgaris

**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

**REFERENCE** 1 (bases 1 to 18)  
Henry, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stehl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelet, U.

**AUTHORS**

**TITLE** Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

**JOURNAL MEDLINE** 22362189

**PUBMED** 12472698

**COMMENT** Contact: Weisshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mp12-koeln.mpg.de

**Insert length:** 18 **Std Error:** 0.00  
**Plate:** 24 **row:** M **column:** 20  
**Seq. primer:** SP6; CATCAGATTAGTGACACTATAG.  
**Location/Qualifiers**

**FEATURES**

**source** 1. 18  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:192416"  
/db\_xref="taxon:161934"  
/clone="024-024-M20"  
/issue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_1ib="MP12-ADIS-024-developing root"  
/note="Vector: pCMVSPORTS; Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfeldener Saatzzucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

**Query Match** 0.3%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1182 AGAAGAGAGAGAGAGA 1198  
|||  
1 AGAAGAGAGAGAGAGA 17

**DB** 1 AGAAGAGAGAGAGAGA 17

**RESULT 481**

**LOCUS** CL436223 19 bp DNA linear GSS 18-MAR-2004

**DEFINITION** PST2544-NR.Seg MICE1 Mus musculus genomic clone PST2544-NR.Seg

**ACCESSION** CL436223

**VERSION** CL436223.1 GI:45570812

**KEYWORDS** GSS.

**SOURCE** Mus musculus (house mouse)

**ORGANISM** Mus musculus

**REFERENCE** 1 (bases 1 to 19)  
Hicks, G.G.

**AUTHORS** www.Escellis.ca

**TITLE** Unpublished (2002)

**JOURNAL** Contact: Hicks GG

**COMMENT** Mammalian Functional Genomics Centre  
Manitoba Institute of Cell Biology, University of Manitoba  
ON S029, 675 McDermot Ave, Winnipeg, MB R3B 0V9, Canada  
Tel: 204 787 2133  
Fax: 204 787 2190  
Email: hicks@cc.manitoba.ca

U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from [http://140.193.242.7/escdb/public\\_search\\_frame.php?PST=PST2544-NR.Seq](http://140.193.242.7/escdb/public_search_frame.php?PST=PST2544-NR.Seq)

**Classes:** Gene Trap.

**FEATURES**

**source** 1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="PST2544-NR.Seg"  
/sex="Male"

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/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 Subclone)"
/clone_lib="MICB1"
/notes="Vector: U3NeoSV1"

Query Match      0.3%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5357 TATAAATTAATAATTT 5373
Db      2 TATTAATTAATAATTTAT 18

RESULT 482
AZ308846/c 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0012H15F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
ACCESSION AZ308846
VERSION AZ308846
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contract: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5393 AAAAAAATACAAAAG 5409
Db      18 AAAAAAATACAAAAG 2

RESULT 483
AB094448 22 bp mRNA linear EST 01-MAY-2003
LOCUS AB094448
DEFINITION AB094448 lambda Triplex2 rice phloem sap cDNA Oryza sativa
(Japonica cultivar-group) cDNA clone P4568, mRNA sequence.
ACCESSION AB094448
VERSION AB094448
KEYWORDS EST.
SOURCE Oryza sativa (Japonica cultivar-group)
ORGANISM Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and
Fujiwara,T.
Small RNAs detected in the rice phloem sap
Unpublished (2003)
Contract: Hironori Mano
Plant Genome Center Co.,Ltd
Kannondai-25-2, Tsukuba, Ibaraki 305-0856, Japan
Tel: 81-298-39-4823
Email: hmano@pgcna.co.jp.
Location/Qualifiers
1..22
/organism="Oryza sativa (Japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="P4568"
/tissue_type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

## Genomics and Bioinformatics

Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII (KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.

## FEATURES

## source

1..20  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C000003\_C23"  
/issue\_type="placenta"  
/clone\_1lb="CSEGRAN09"  
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 TAAAAAATACAAAAAGAA 5412

DB 20 TAAAAAATACAAAAAGAA 1

## RESULT 485

AL038427 20 bp mRNA linear EST 06-JUL-2004  
LOCUS DKFZP566A1946\_r1 566 (synonym: hfkdx2) Homo sapiens cDNA clone  
DEFINITION DKFZP566A1946, mRNA sequence.  
ACCESSION AL038427  
VERSION AL038427.1 GI:49682121  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566A1946"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

## FEATURES

## source

1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566A1946"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAAGAA 5411

DB 1 TAAAAAATACAAAAAGAA 20

## RESULT 486

AL038429

AL038429 20 bp mRNA linear EST 06-JUL-2004  
LOCUS DKFZP566A1946\_r1 566 (synonym: hfkdx2) Homo sapiens cDNA clone  
DEFINITION DKFZP566A1946, mRNA sequence.

ACCESSION AL038429  
VERSION AL038429.1 GI:49682123  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566A1946"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

## FEATURES

## source

1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566A1946"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAAGAA 5411

DB 1 TAAAAAATACAAAAAGAA 20

RESULT 487  
AL038507 20 bp mRNA linear EST 06-JUL-2004  
LOCUS DKFZP566D1846\_r1 566 (synonym: hfkdx2) Homo sapiens cDNA clone  
DEFINITION DKFZP566D1846, mRNA sequence.  
ACCESSION AL038507  
VERSION AL038507.1 GI:49682146  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Ostenwaelder, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.  
Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566D1846"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

## FEATURES

## source

1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP566D1846"  
/issue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1lb="566 (synonym: hfkdx2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

## Query Match

0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTAATAATACAAAGAA 5410  
|||||  
Db 1 TTAATAATACAAAGAA 20

RESULT 488  
AL038570

LOCUS AL038570 20 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566F1746.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566F1746, mRNA sequence.

VERSION AL038570

KEYWORDS AL038570.1 GI:49682159

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 20)

Ostenwaeelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

Wiemann, S. (Ostenwaeelder, et al.)

TITLE EST (Ostenwaeelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..20

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZP566F1746"

/tissue\_type="kidney"

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/lab\_host="X1-2blue"

/clone\_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1, Site\_1: NotI; Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5392 TAAATAATACAAAGAA 5411  
|||||  
Db 1 TAAATAATACAAAGAA 20

RESULT 489  
AL038576

LOCUS AL038576 20 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566F0346.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566F0346, mRNA sequence.

VERSION AL038576

KEYWORDS AL038576.1 GI:49682161

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 20)

Ostenwaeelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

Wiemann, S. (Ostenwaeelder, et al.)

TITLE EST (Ostenwaeelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..20

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZP566F0346"

/tissue\_type="kidney"

/dev\_stage="fetal"

/lab\_host="X1-2blue"

/clone\_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1, Site\_1: NotI; Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTAATAATACAAAGAA 5410  
|||||  
Db 1 TTAATAATACAAAGAA 20

RESULT 490  
AL038750

LOCUS AL038750 20 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566M1146.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566M1146, mRNA sequence.

VERSION AL038750

KEYWORDS AL038750.1 GI:49682199

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 20)

Ostenwaeelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

Wiemann, S. (Ostenwaeelder, et al.)

TITLE EST (Ostenwaeelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..20

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZP566M1146"

/tissue\_type="kidney"

/dev\_stage="fetal"

/lab\_host="X1-2blue"

/clone\_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1, Site\_1: NotI; Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAATACAAAGAA 5412  
|||||  
Db 1 AAAAAAATACAAAGAA 20

RESULT 491  
AL038754

LOCUS AL038754 20 bp mRNA linear EST 06-JUL-2004  
DEFINITION DKFZP566M1346.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566M1346, mRNA sequence.

VERSION AL038754

KEYWORDS AL038754.1 GI:49682201

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 20)

Ostenwaeelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

Wiemann, S. (Ostenwaeelder, et al.)

TITLE EST (Ostenwaeelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..20

/organism="Homo sapiens"

/mol\_type="mRNA"

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TITLE      EST (Ottewaeider, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
ORGANISM   MIPS
FEATURES   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
            Location/Qualifiers
            1..20
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp566M1346"
            /issue_type="kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_1lb="566 (synonym: hfk22)"
            /note="Vector: pMPL; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 85.0%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAGAG 5410
|||||
1 TTTAAAAAATACAAAAGAG 20

RESULT 492
AL038845 20 bp mRNA linear EST 06-JUL-2004
LOCUS    DKFZp566P1746.r1.566 (synonym: hfk22) Homo sapiens cDNA clone
DEFINITION
ACCESSION AL038845
VERSION    AL038845.1 GI:49682220
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 20)
            Ottewaeider, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
            Wiemann, S.
            EST (Ottewaeider, et al.)
            Unpublished (1999)
            Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
            Location/Qualifiers
            1..20
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp566P1746"
            /issue_type="kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_1lb="566 (synonym: hfk22)"
            /note="Vector: pMPL; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 85.0%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAGAG 5410
|||||
1 TTTAAAAAATACAAAAGAG 20

RESULT 493
AL587630 20 bp mRNA linear EST 02-MAR-2001
LOCUS    AL587630 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION
ACCESSION AL587630
            ROS060A07, mRNA sequence.
            AL587630

```

```

VERSION    AL587630.1 GI:13192664
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 20)
            Murray, P.
            BP Chicken Brain Library
            Unpublished (2001)
            Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@birc.ac.uk
            GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
            (*6854-
            (*6854-
            Seq primer: M13P.
            Location/Qualifiers
            1..20
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /db_xref="taxon:9031"
            /clone="ROS060A07"
            /issue_type="Brain"
            /dev_stage="Unknown"
            /lab_host="DH10B"
            /clone_1lb="BP Chicken Brain Library"
            /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
            unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
            5' TCGACCTGAG 3' ; 3' adaptor sequence: 5'
            GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
            Clontech (*6854-1)"

Query Match
Best Local Similarity 85.0%; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAATGCAAAAT 5422
|||||
20 AAAAAAGAAAATGCAAAAT 1

RESULT 494
AM334823 20 bp mRNA linear EST 31-JAN-2000
LOCUS    AM334823
DEFINITION AM334823 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AM334823
VERSION    AM334823.1 GI:6831180
KEYWORDS   EST.
SOURCE     Pneumocystis carinii
            Pneumocystis carinii
            Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
            1 (bases 1 to 20)
            Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
            Edman, J.C., Kovacs, J. and Cushion, M.
            Expressed sequence tags from Pneumocystis carinii
            Unpublished (2000)
            Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
            Location/Qualifiers
            1..20
            /organism="Pneumocystis carinii"

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/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_1ib="AGS-1"  
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
P. carinii organisms (3x10es) from a single rat (59-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dt priming, standard  
conditions described by vendor. Stratagene. Further  
details see www.uky.edu/project/Pneumocystis/"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAA 5412  
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 495  
CF280913 20 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,  
mRNA sequence.  
ACCESSION CF280913 GI:33658299  
VERSION CF280913  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..20  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ETL--07-M07"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1ib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAA 5412  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 496  
CF282035

LOCUS CF282035 20 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,  
mRNA sequence.  
ACCESSION CF282035 GI:33659422  
VERSION CF282035  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..20  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/clone="14ETL--09-F19"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1ib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAA 5412  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 497  
CF282414 20 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ETL--09-019.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-019,  
mRNA sequence.  
ACCESSION CF282414 GI:33659801  
VERSION CF282414  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

1.20 /organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39347"

/clone="14ESTL--09-019"

/issue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice etiolated leaf plasmid cDNA library (14ESTL)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0.3%; Score 15.2; DB 1; Length 20;

5393 AATTAATAATCAAAAAA 5412

1 AAAAAAAAAAAAAAAAAA 20

RESULT 498

CP298018

7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION

sequence.

CP298018

CP298018.1 GI:33669779

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1.20

Db

20 AATCAAAAAAAAAAAAAA 1

RESULT 499

CP299822/c

LOCUS

DEFINITION

sequence.

CP299822

CP299822.1 GI:33671583

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1.20

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39347"

/clone="7LEAF--03-P22"

/issue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0.3%; Score 15.2; DB 1; Length 20;

5393 AATTAATAATCAAAAAA 5412

20 AAAAAAAAAAAAAAAAAA 1

RESULT 500

CP301720/c

LOCUS

DEFINITION

sequence.

CP301720

CP301720.1 GI:33673481

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1.20

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39347"

/clone="7LEAF--06-L01"

/issue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0.3%; Score 15.2; DB 1; Length 20;

5393 AATTAATAATCAAAAAA 5412

20 AAAAAAAAAAAAAAAAAA 1

RESULT 500

CP301720/c

LOCUS

DEFINITION

sequence.

CP301720

CP301720.1 GI:33673481

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 3;

## QY

5393 AAAAAATACAAAAAGAAA 5412

## Db

20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 501  
CF302027/c 20 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA  
sequence.

## ACCESSION

CF302027.1 GI:33673788

## VERSION

CF302027

## KEYWORDS

EST.

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 20)

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
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Best Local Similarity 85.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 3;

## QY

5393 AAAAAATACAAAAAGAAA 5412

## Db

20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 502  
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LOCUS ABR--03-A01.g1 ABR3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABR--03-A01, mRNA sequence.

## ACCESSION

CF308984.1 GI:33680745

## VERSION

CF308984

## KEYWORDS

EST.

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 20)

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

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line."
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5389 AATTAAAAAATACAAAAA 5408

## Db

20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 503  
CF310604 20 bp mRNA linear EST 15-AUG-2003  
LOCUS ABR--05-F14.g1 ABR3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABR--05-F14, mRNA sequence.

## ACCESSION

CF310604.1 GI:33682365

## VERSION

CF310604

## KEYWORDS

EST.

## SOURCE

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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line."

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 504  
CFJ13067  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CFJ13067 20 bp mRNA linear EST 15-AUG-2003  
HD--01-B02.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--01-B02, mRNA sequence.  
CFJ13067  
CFJ13067.1 GI:33684828  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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line."

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATGCAAAAAGAAA 5412  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 505  
CFJ13569/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CFJ13569 20 bp mRNA linear EST 15-AUG-2003  
HD--01-L22.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--01-L22, mRNA sequence.  
CFJ13569  
CFJ13569.1 GI:33685330  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
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derived from rice Histone Deacetylase overexpression  
line."

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT	506
CESL9133/c	
LOCUS	CFJ19133
DEFINITION	HD--09-113.b1 OsHDACT1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa [japonica cultivar-group] cDNA clone HD--09-113, mRNA sequence.
ACCESSION	CFJ19133
VERSION	CFJ19133.1 GI:33690894
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 20) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoung University Yongin, Kyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnah@gpbio.com, bhnah@bio.myonji.ac.kr.  location/Qualifiers
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RESULT	507
LOCUS	CFJ321721/c
DEFINITION	CFJ321721
ACCESSION	CFJ321721.1 GI:33693482
VERSION	EST.
KEYWORDS	Oryza sativa (japonica cultivar-group)
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eshartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 20) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analaysis of Rice ESTs Unpublished (2003)
TITLE	JOURNAL

```

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.3% Score 15.2; DB 1; Length 20;
Beet Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

Oy      5393 AAAAAATACAAAAGGAA 5412
         ||||| | ||||| |||
Db       20 AAAAAAAAAAAAAAAAAA 1

RESULT 508
CFJ28565
LOCUS     CFJ28565
DEFINITION NACL--03-114.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-114, mRNA
          sequence.
ACCESSION CFJ28565
VERSION   CFJ28565
KEYWORDS  CFJ28565.1 GI:33805376
SOURCE    ERT.
ORGANISM  Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoidae; Oryzaceae; Oryza.
          1 (bases 1 to 20)
          Kim,J.S., Jun,K.M., Cheong,P.U., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, Greengene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 509  
 CF331173 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF331173/c  
 DEFINITION JMT--01-P11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--01-P11, mRNA sequence.

ACCESSION CF331173 GI:33814617

VERSION CF331173  
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Bukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
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 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
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 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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RESULT 510  
 CF331170 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF331170/c  
 DEFINITION JMT--03-P17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--03-P17, mRNA sequence.

ACCESSION CF331170 GI:33816671

VERSION CF331170  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
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 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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 source Location/Qualifiers

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 methyltransferase overexpression line."

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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 511  
 CF336525/c 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF336525/c  
 DEFINITION JMT--06-J21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--06-J21, mRNA sequence.

ACCESSION CF336525 GI:33821425

VERSION CF336525  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Bukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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 Unpublished (2003)  
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 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412  
 DB 20 AAAAAAAAAAAAAAAAAA 1

RESULT 512  
 CF337494/c 20 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF337494/c  
 DEFINITION JMT--07-P04.g1 AtUMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone  
 JMT--07-P04, mRNA sequence.  
 CF337494  
 ACCESSION CF337494.1 GI:33823378  
 VERSION  
 KEYWORDS  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriactoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahn B.H.  
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 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 Location/Qualifiers  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="JMT--07-P04"  
 /issue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1lb="AtUMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis thaliana Carboxyl  
 methyltransferase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412  
 DB 20 AAAAAAAAAAAAAAAAAA 1

RESULT 513  
 CN545446/c 20 bp mRNA linear EST 30-APR-2004  
 LOCUS CN545446/c  
 DEFINITION EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera cDNA  
 clone B3C8006L005C02 3', mRNA sequence.  
 CN545446  
 ACCESSION CN545446.1 GI:46910071  
 VERSION  
 KEYWORDS  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 20)  
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,  
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,  
 Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
 or seeds) at Various Developmental Stages  
 Unpublished (2002)  
 CONTACT: Hamdi S.  
 UMR 619 - Equipe Biologie de la Vigne  
 Universite de Bordeaux I, Institut National de la Recherche  
 Agronomique  
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
 France  
 Tel: 00-33-(0)5-57-12-25-50  
 Fax: 00-33-(0)5-57-12-25-48  
 Email: s.hamdi@bordeaux.inra.fr  
 Seq primer: 17.  
 Location/Qualifiers  
 1..20  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3C8006L005C02"  
 /dev\_stage="green stage"  
 /clone\_1lb="Green Grape Skin Triplex2 Library"  
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
 SfilI; Site\_2: SfilI; Oriented library"

FEATURES  
 source  
 1..20  
 Location/Qualifiers  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Cabernet Sauvignon"  
 /db\_xref="taxon:29760"  
 /clone="B3C8006L005C02"  
 /dev\_stage="green stage"  
 /clone\_1lb="Green Grape Skin Triplex2 Library"  
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
 SfilI; Site\_2: SfilI; Oriented library"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412  
 DB 20 AAAAAAAAAAAAAAAAAA 1

RESULT 514  
 CN545501/c 20 bp mRNA linear EST 30-APR-2004  
 LOCUS CN545501/c  
 DEFINITION EST 17445 Green Grape Skin Triplex2 Library Vitis vinifera cDNA  
 clone B3C8006L005H02 3', mRNA sequence.  
 CN545501  
 ACCESSION CN545501.1 GI:46910126  
 VERSION  
 KEYWORDS  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 20)  
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,  
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,  
 Hamdi,S., Romieu,C. and Terrier,N.  
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
 or seeds) at Various Developmental Stages  
 Unpublished (2002)  
 CONTACT: Hamdi S.  
 UMR 619 - Equipe Biologie de la Vigne

QY 5393 AAAAAAAAAAAGAAA 5412  
 DB 20 AAAAAAAAAAAAAAAAAA 1

Universite de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
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Tel: 00-33 - (0)5-57-12-25-50  
Fax: 00-33 - (0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: T7  
Location/Qualifiers

FEATURES  
source  
1..20  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
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/db\_xref="taxon:29760"  
/clone="B3C800C0405H02"  
/dev\_stage="green stage"  
/clone\_1lb="Green Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
Sf1A; Site\_2: Sf1B; Oriented library"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412  
|||||  
20 AAAAAAAAAAAAAAAAAA 1

RESULT 515  
T50579/c 20 bp mRNA 1linear EST 06-FEB-1995  
DEFINITION yb76d04.r1 Stratiogene ovary (#937217) Homo sapiens cDNA clone  
IMAGS:77095 5' similar to contains 11 repetitive element, mRNA  
sequence.  
T50579  
T50579.1 GI:652439  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 20)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chapelli, B.,  
Chisoe, S., Dietrich, N., Dubaque, T., Favello, A., Gish, W.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,  
Marila, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,  
Rohlfing, T., Scheilenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,  
Trevaskis, B., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
and Marra, M., Generation and analysis of 280,000 human expressed sequence tags

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watscn.mucsl.edu  
Source: IMAGB Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGB Consortium (info@image.lnl.gov) for further information.  
Seq primer: M13RP1  
High quality sequence stop: 21.  
Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:506824"  
/db\_xref="taxon:9606"  
/clone="IMAGB:77095"  
/sex="female"

FEATURES  
source  
1..20  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:506824"  
/db\_xref="taxon:9606"  
/clone="IMAGB:77095"  
/sex="female"

/dev stage="49 year old"  
/lab host="SOLR cells (kanamycin resistant)"  
/clone\_1lb="Stratiogene ovary (#937217)"  
/note="Organ: ovary; Vector: Bluescript SK; Site\_1: EcoRI;  
Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo dt.  
Total ovary tissue, normal, caucasian. Average insert  
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'  
GAATCGGACGAG 3' -3' adaptor sequence: 5'  
CTCGAGTTTTTTTTTTTTTTT 3'."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412  
|||||  
20 AAAAAAAAAAAAAAAAAA 1

RESULT 516  
AZ307671/c 20 bp DNA 1linear GSS 29-SEP-2000  
DEFINITION 1M0009M20R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0009M20 R, genomic survey sequence.  
AZ307671  
AZ307671.1 GI:10346897  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: M column: 20  
Seq primer: CACACAGGAAACAGCATGACG  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0009M20"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

FEATURES  
source  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0009M20"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electroporation. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 517  
A2333980 20 bp DNA linear GSS 29-SEP-2000  
LOCUS A2333980/c Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0063K10 F, genomic survey sequence.  
ACCESSION A2333980  
VERSION A2333980.1 GI:10400856  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0063 row: K column: 10  
Seq primer: CGTGTAAACACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20

FEATURES  
source

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0063K10"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 518  
A2341237 20 bp DNA linear GSS 29-SEP-2000  
LOCUS A2341237 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0073G03 R, genomic survey sequence.  
ACCESSION A2341237  
VERSION A2341237.1 GI:10417288  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: G column: 03  
Seq primer: CACACAGAAACAGTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20

FEATURES  
source

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0073G03"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number



Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No.3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5397 AATATCAAAAAGAAAAAT 5416  
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1 AAAAAAAAAAAAAAAAAAAT 20

Db 1 AAAAAAAAAAAAAAAAAAAT 20

#### RESULT 519

AZ341530 20 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0073N21R Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0073N21 R, genomic survey sequence.

ACCESSION AZ341530.1 GI:10417873

VERSION AZ341530.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: N column: 21

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No.3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAA 20

Db 1 AAAAAAAAAAAGAAA 20

#### RESULT 520

AZ343031 20 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0076F13F Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0076F13 F, genomic survey sequence.

ACCESSION AZ343031.1 GI:10420861

VERSION AZ343031.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: F column: 13

Seq primer: CATTGTAAAACGACGCGACT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No.3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAA 20

Db 1 AAAAAAAAAAAGAAA 20

#### RESULT 520

AZ343031 20 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0076F13F Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0076F13 F, genomic survey sequence.

ACCESSION AZ343031.1 GI:10420861

VERSION AZ343031.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: F column: 13

Seq primer: CATTGTAAAACGACGCGACT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No.3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No.3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAA 20

Db 1 AAAAAAAAAAAGAAA 20

#### RESULT 520

AZ343031 20 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0076F13F Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0076F13 F, genomic survey sequence.

ACCESSION AZ343031.1 GI:10420861

VERSION AZ343031.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: F column: 13

Seq primer: CATTGTAAAACGACGCGACT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5393 AAAAAATACAAAAAGAAA 5412  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 521  
AZ343730/c 20 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0077E20 F, genomic survey sequence.

ACCESSION AZ343730  
VERSION AZ343730.1 GI:10422288  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0077 row: B column: 20  
Seq primer: CGTTGTAAAACGACGGCAGT  
Class: plasmid ends

High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source 1..20

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0077E20"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5395 AAAAAATACAAAAAGAAA 5414  
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 522  
AZ351273 20 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0089B18 F, genomic survey sequence.

ACCESSION AZ351273  
VERSION AZ351273.1 GI:10430510  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0089 row: B column: 18  
Seq primer: CGTTGTAAAACGACGGCAGT  
Class: plasmid ends

High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source 1..20

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0089B18"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 523

AZ357623

LOCUS

DEFINITION

1M0099A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ357623

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0099A20"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

20 bp DNA linear GSS 02-OCT-2000  
clone UUGC1M0099A20 F, genomic survey sequence.  
GSS.  
AZ357623.1 GI:10471335  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0099 row: A column: 20  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1.20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0099A20"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 524

AZ369734

LOCUS

DEFINITION

1M0120024F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ369734

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0120024"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

20 bp DNA linear GSS 02-OCT-2000  
clone UUGC1M0120024 F, genomic survey sequence.  
GSS.  
AZ369734.1 GI:10483434  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0120 row: O column: 24  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1.20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0120024"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 525

A2386573

LOCUS A2386573 20 bp DNA linear GSS 02-OCT-2000

DEFINITION 1M0145C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0145C11 R, genomic survey sequence.

ACCESSION A2386573

VERSION A2386573.1 GI:10500273

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0145 row: C column: 11

Seq primer: CACACGGAACACGCTATAC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0145C11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 526

A2396481

LOCUS A2396481 20 bp DNA linear GSS 03-OCT-2000

DEFINITION 1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0161K02 F, genomic survey sequence.

ACCESSION A2396481

VERSION A2396481.1 GI:10511553

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0161 row: K column: 02

Seq primer: CATTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0161K02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 527

AZ405596 20 bp DNA linear GSS 03-OCT-2000

LOCUS 1M0174B06R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0174B06 R, genomic survey sequence.

ACCESSION AZ405596

VERSION AZ405596.1 GI:10529609

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0174 row: B column: 06

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0174B06"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4146 AAACCCAGCTTCTCCCT 4165

Db 20 AAACCCAGCTTCTCCCT 1

## RESULT 528

AZ442328

LOCUS 1M0236B11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0236B11 F, genomic survey sequence.

ACCESSION AZ442328

VERSION AZ442328.1 GI:10566341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: B column: 11

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0236B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4146 AAACCCAGCTTCTCCCT 4165

Db 20 AAACCCAGCTTCTCCCT 1

## RESULT 528

AZ442328

LOCUS 1M0236B11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0236B11 F, genomic survey sequence.

ACCESSION AZ442328

VERSION AZ442328.1 GI:10566341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: B column: 11

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0236B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4146 AAACCCAGCTTCTCCCT 4165

Db 20 AAACCCAGCTTCTCCCT 1

## RESULT 528

AZ442328

LOCUS 1M0236B11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0236B11 F, genomic survey sequence.

ACCESSION AZ442328

VERSION AZ442328.1 GI:10566341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

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University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: B column: 11

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0236B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4146 AAACCCAGCTTCTCCCT 4165

Db 20 AAACCCAGCTTCTCCCT 1

## RESULT 528

AZ442328

LOCUS 1M0236B11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0236B11 F, genomic survey sequence.

ACCESSION AZ442328

VERSION AZ442328.1 GI:10566341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

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University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: B column: 11

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0236B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4146 AAACCCAGCTTCTCCCT 4165

Db 20 AAACCCAGCTTCTCCCT 1

## RESULT 528

AZ442328

LOCUS 1M0236B11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

DEFINITION clone UGCGIM0236B11 F, genomic survey sequence.

ACCESSION AZ442328

VERSION AZ442328.1 GI:10566341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: B column: 11

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0236B11"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end

QY 5393 AAAAAAAAAACAAAGAAA 5412  
 |||||  
 DB 1 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 529  
 A2463331 20 bp DNA linear GSS 04-OCT-2000  
 LOCUS A2463331/C  
 DEFINITION 1M0272006F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 clone UUCG1M0272006 F, genomic survey sequence.

ACCESSION A2463331  
 VERSION A2463331.1 GI:10621456  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0272 row: 0 column: 06  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0272006"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412  
 |||||  
 DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 530  
 A2477734 20 bp DNA linear GSS 04-OCT-2000  
 LOCUS A2477734/C  
 DEFINITION 1M0297E23F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 clone UUCG1M0297E23 F, genomic survey sequence.

ACCESSION A2477734  
 VERSION A2477734.1 GI:10635978  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0297 row: E column: 23  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0297E23"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412



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RESULT 533
AZ46787/c
LOCUS      AZ46787          20 bp    DNA        linear   GSS 05-OCT-2000
DEFINITION ClONE J15D23F Mouse 10kb plasmid U09C1M library Mus musculus genomic
ACCESSION  J15D23F
VERSION     AZ46787
KEYWORDS    AZ46787.1  GI:10653904
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   Eukaryote; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 20)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE       Unpublished (2000)
JOURNAL     Contact: Robert B. Weiss
COMMENT     University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0315 row: D column: 23
            Seq primer: CGTGTGTAACAGCACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES
source
location/Qualifiers
1..20
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/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="U09C1M0315D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid U09C1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred.No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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	RESULT	534
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LOCUS	20 bp DNA linear GSS 05-OCT-2000	
DEFINITION	IM033BE05F Mouse 10kb plasmid UUGCJM library Mus musculus genomic clone UUGCJM033BE05 F, genomic survey sequence.	
ACCESSION	AZ498625	
VERSION	AZ498625.1 GI:10676657	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus. 1 (bases 1 to 20) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Department of Biology Room 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0336 row: R column: 05 Seq primer: CGTTGTAACAAGCGAGCCACT Class: plasmid ends High quality sequence stop: 20. Location/Qualifiers 1..20 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCJM033BE05" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lid="Mouse 10kb plasmid UUGCJM library" /note="Vector: pMD2env, purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 [GI473114[bp]AP129072.1], a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
Query Match	0.3%; Score 15.2;	DB 1; Length 20;
Best Local Similarity	85.0%;	Pred. No. 3.3e+02;
Matches 17; Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
CY	5393 AAAAATACAAAAGA 5412	
DB	AAAAAAAAAAAAAAAAAA 1	



## RESULT 535

AZ514729

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

20 bp DNA linear GSS 05-OCT-2000

1M0361B1R1R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone UGCG1M0361B1R1 R, genomic survey sequence.

AZ514729

AZ514729.1 GI:10696045

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhuesern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: B column: 11

Seq primer: CACACAGAAACAGCATATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG1M0361B1R1"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 AAAAAAAAAAAAAAAAAA 5412

RESULT 536

## AZ579122

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

20 bp DNA linear GSS 13-DEC-2000

1M0363G19F Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone UGCG1M0363G19 F, genomic survey sequence.

AZ579122

AZ579122.1 GI:11693583

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhuesern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

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Seq primer: CGTGTGAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/clone\_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 AAAAAAAAAAAAAAAAAA 5415

RESULT 537

AZ579178

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 VERSION AZ579178  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 Plate: 0363 row: F column: 11  
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 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
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 adaptor DNA was purified and size-selected for a 9.5 to  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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 Db 1 CAAAAAAGAAAAA 20

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DEFINITION IM0369P15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0369P15 R, genomic survey sequence.  
 ACCESSION AZ581208  
 VERSION AZ581208  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 High quality sequence stop: 20.  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
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QY 5393 AAAAAATTCAAAAAGAAA 5412  
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 Db 1 AAAAAA 20

RESULT 539  
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 LOCUS  
 DEFINITION IM0396A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION clone UGSC1W0396A13 F, genomic survey sequence.  
 VERSION A2588011  
 KEYWORDS A2588011.1 GI:11710297  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Molecule Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Baicorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid insets  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel.: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 Class: plasmid ends  
 High quality sequence atop: 20.  
 Location/Qualifiers  
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 source

Query Match	0.3%	Score 15.2	DB 1	Length 20
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ACCESSION	AZ607328
VERSION	AZ607328.1
KEYWORDS	GI:11729518
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ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 20) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Jellam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright D.Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0429 row: A column: 14 Seq primer: CACACAGAAACACGCTATGACC Class: plasmid ends High quality sequence stop: 20. location/Qualifiers 1..20
FEATURES	
SOURCE	

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Query Match          0.3% Score 15.2 DB 1 Length 20;
Best Local Similarity 85.0% Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION clone UGCGIM0460K05 R, genomic survey sequence.
ACCESSION  A2623155

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VERSION AZ623155.1 GI:11745345  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412  
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DEFINITION clone UUCG1M0460L12 R, genomic survey sequence.  
ACCESSION AZ623214  
VERSION AZ623214.1 GI:11745404

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 20 AAAAAAAAAAAAAAAAAAAAA 1

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DEFINITION clone UUCG1M0507D18 R, genomic survey sequence.  
ACCESSION AZ643992  
VERSION AZ643992.1 GI:11772092  
KEYWORDS GSS.

**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**  
Mus musculus

**REFERENCE**  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

**AUTHORS**  
Niederhausern, A. and Wright, D., Weis, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Plate: 0507 row: D column: 18  
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**Query Match**  
Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 5393 AAAAAAAAAACAAAGAAA 5412  
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DEFINITION clone UUGC1M0511003 R, genomic survey sequence.  
ACCESSION AZ645829  
VERSION AZ645829.1 GI:11775703  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

**ORGANISM**  
Mus musculus

**REFERENCE**  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

**AUTHORS**  
Niederhausern, A. and Wright, D., Weis, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0511 row: D column: 03  
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Class: plasmid ends  
High quality sequence stop: 20.

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**Query Match**  
Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 5393 AAAAAAAAAACAAAGAAA 5412  
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ACCESSION AZ650271  
VERSION AZ650271.1 GI:11784588  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## TITLE

Unpublished (2000)

JOURNAL  
COMMENT

Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0520 row: C column: 21  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAA 20

## RESULT 546

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LOCUS A2760838 20 bp DNA linear GSS 16-FEB-2001

DEFINITION 1M055424R Mouse 10kb plasmid UUC1M library Mus musculus genomic

## ACCESSION

## A2760838

VERSION A2760838.1 GI:12869112

## KEYWORDS

## GSS.

Mus musculus (house mouse)

## SOURCE

Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## TITLE

Unpublished (2000)

JOURNAL  
COMMENT

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Tel: 801 585 5606  
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Email: ddunne@genetics.utah.edu  
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## FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAA 20

## RESULT 547

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LOCUS A2764504 20 bp DNA linear GSS 16-FEB-2001

DEFINITION 1M0560M02R Mouse 10kb plasmid UUC1M library Mus musculus genomic

## ACCESSION

A2764504

VERSION A2764504.1 GI:12879535

## KEYWORDS

## GSS.

Mus musculus (house mouse)

## SOURCE

Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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QY 5393 AAAAAAATCAAAAAAGAA 5412  
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 Db 1 AAAAAAAAAAAAAAAAAA 20

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 accession AZ765211  
 version AZ765211.1 GI:12880970  
 keywords GSS.  
 source Mus musculus (house mouse)  
 organism Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 reference 1 (bases 1 to 20)  
 authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
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 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATCAAAAAAGAA 5412  
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 Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 549  
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 DEFINITION 1M0574A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
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 version AZ772091.1 GI:12895040  
 keywords GSS.  
 source Mus musculus (house mouse)  
 organism Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 reference 1 (bases 1 to 20)  
 authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
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Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0574 row: A column: 13  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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0.005 inch orifice at constant velocity. The sheared DNA  
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with adaptors complementary to the insert adaptors and  
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chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAATCAAAAAAAAAAGAA 5412  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

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clone UUGC2M0015M18 R, genomic survey sequence.  
ACCESSION  
A2779425  
VERSION  
A2779425.1 GI:12910066  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
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plasmid inserts  
Unpublished (2000)  
JOURNAL  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0015 row: M column: 18  
Seq primer: CACACAGGAAACAGCTATGACC  
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High quality sequence stop: 20.  
Location/Qualifiers

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/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAAAAAATCAAAAAAAAAAGAA 5412  
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Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

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DEFINITION 2M0026B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0026B21 F, genomic survey sequence.  
ACCESSION  
A2784041  
VERSION  
A2784041.1 GI:12919375  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von



TITLE Niederhauserm, A. and Wright, D., Weiss, R.  
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb  
 COMMENT plasmid inserts  
 Unpublished (2000)  
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 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0026 row: B column: 21  
 Seq primer: CGTGTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.

# FEATURES

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 /mol\_type="genomic DNA"  
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 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAGAAA 5412  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 552  
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 DEFINITION clone UUGC2M0046C16 R, genomic survey sequence.  
 ACCESSION AZ793467  
 VERSION AZ793467.1 GI:12938450  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
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 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauserm, A. and Wright, D., Weiss, R.

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 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0046 row: C column: 16  
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 Class: plasmid ends  
 High quality sequence stop: 20.

# FEATURES

source  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAGAAA 5412  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 553  
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 ACCESSION AZ798529  
 VERSION AZ798529.1 GI:12948718  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauserm, A. and Wright, D., Weiss, R.  
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JOURNAL  
COMMENT

plasmid inserts  
Unpublished (2000)  
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Insert Length: 10000 Std Error: 0.00  
Plate: 0055 row: G column: 19  
Seq primer: CATTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
http://www.jax.org/resources/documents/dnares/. The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412  
|||||  
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

## RESULT 554

AZ805163 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0066114F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0066114 F, genomic survey sequence.  
ACCESSION AZ805163  
VERSION AZ805163.1 GI:12965890  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0066 row: L column: 14  
Seq primer: CATTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0066L14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
http://www.jax.org/resources/documents/dnares/. The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 20

## RESULT 555

AZ806521 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0068C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0068C08 R, genomic survey sequence.  
ACCESSION AZ806521  
VERSION AZ806521.1 GI:12969953  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0068 row: C column: 08  
Seq primer: CACACAGAAACGCTATACCC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. 20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0068C08"  
/sex="Male"  
/lab\_host="R. Colt strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 556  
AZ806585  
LOCUS 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0068C15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M0068C15 R, genomic survey sequence.  
ACCESSION AZ806585  
VERSION AZ806585.1 GI:12970081  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0068 row: C column: 15  
Seq primer: CACACAGAAACGCTATACCC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. 20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0068C15"  
/sex="Male"  
/lab\_host="R. Colt strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 557  
AZ809306  
LOCUS 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0073D15F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M0073D15 F, genomic survey sequence.  
ACCESSION AZ809306  
VERSION AZ809306.1 GI:12975468  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: D column: 15  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U06C2M0073D15"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid U06C1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412  
|||||  
DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 558  
AZ810986 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0076120R Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C2M0076120 R, genomic survey sequence.

ACCESSION AZ810986  
VERSION AZ810986.1 GI:12978793  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

JOURNAL Contact: Robert B. Weis

COMMENT University of Utah  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: I column: 20  
Seq primer: CACACAGGAACAGCTAGACC  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

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1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U06C2M0076120"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid U06C1M library"

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412  
|||||  
DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 559  
AZ813908 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0081P21F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C2M0081P21 F, genomic survey sequence.

ACCESSION AZ813908  
VERSION AZ813908.1 GI:12983804  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

JOURNAL Contact: Robert B. Weis

COMMENT University of Utah  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0081 row: F column: 21  
 Seq primer: CCGTGTAAACGACGCCAGCT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

## FEATURES

source

1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U082M0081P21"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Cyt 5393 AAAAAATTCAGAAAAGAA 5412  
 Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 560  
 AZ817323 20 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0086C20R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG2M0086C20 R, genomic survey sequence.  
 ACCESSION AZ817323  
 VERSION AZ817323.1 GI:12987327  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0081 row: C column: 20  
 Seq primer: CACACGAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

## FEATURES

source

1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U082M0086C20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Cyt 5393 AAAAAATTCAGAAAAGAA 5412  
 Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 561  
 AZ817414 20 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0086K08R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG2M0086K08 R, genomic survey sequence.  
 ACCESSION AZ817414  
 VERSION AZ817414.1 GI:12987328  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0086 row: K column: 08  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

## FEATURES

source

1. .20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG2M0086J15"  
 /sex="Male"  
 /lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 562

AZ817467

LOCUS AZ817467 20 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0086J15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 clone UUCG2M0086J15 R, genomic survey sequence.

ACCESSION AZ817467  
 VERSION AZ817467.1 GI:12987291  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0086 row: J column: 15  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

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 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 563

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 clone UUCG2M0087K08 F, genomic survey sequence.

ACCESSION AZ817608  
 VERSION AZ817608.1 GI:12987516  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00  
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Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

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/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

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clone UUCG2M0088K01 R, genomic survey sequence.  
ACCESSION A2818489  
VERSION A2818489.1 GI:12988397  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00

Plate: 0088 row: K column: 01  
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Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

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/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

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DEFINITION 2M0089M05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG2M0089M05 F, genomic survey sequence.  
ACCESSION A2818816  
VERSION A2818816.1 GI:12988724  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0089 row: M column: 05

Seq primer: CGTTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUCG1M library"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412  
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Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 566  
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LOCUS 2M0132K13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG2M0132K13 R, genomic survey sequence.  
ACCESSION AZ837491  
VERSION AZ837491.1 GI:13007399  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
REFERENCE 1 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0132 row: K column: 13  
Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412  
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Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 567  
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LOCUS 2M0139H16F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG2M0139H16 F, genomic survey sequence.  
ACCESSION AZ841342  
VERSION AZ841342.1 GI:13011250  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
REFERENCE 1 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0139 row: H column: 16  
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Class: plasmid ends



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High quality sequence stop: 20.  
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/note="Vector: PWD42nV, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Cy 5393 AAAAAAAAAACAAAAA 5412  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 568  
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DEFINITION clone UUGC2M0139A10 R, genomic survey sequence.  
ACCESSION AZ841558  
VERSION AZ841558.1 GI:13011466  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nV, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DEFINITION clone UUGC2M0150P21 R, genomic survey sequence.  
ACCESSION AZ849506  
VERSION AZ849506.1 GI:13033596  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0150 row: P column: 21  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
FEATURES  
Location/Qualifiers

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/clone="U062M0150P21"
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/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAATATCAAAAAAGA 5410  
Db 1 TTTAAAAATATCAAAAAAGA 20

RESULT 570  
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DEFINITION clone U062M0150P21 F, genomic survey sequence.  
ACCESSION A2858052  
VERSION A2858052.1 GI:13050813  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0163 row: 0 column: 03  
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High quality sequence stop: 20.  
Location/Qualifiers 1..20

FEATURES  
Source

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/clone="U062M0150P21"
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/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATATCAAAAAAGA 5412  
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A2858419 20 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0163003R Mouse 10kb plasmid U062M0150P21  
DEFINITION clone U062M0150P21 R, genomic survey sequence.  
ACCESSION A2858419  
VERSION A2858419.1 GI:13051545  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0163 row: 0 column: 03  
Seq primer: CACACAGGAAACAGCTAGAC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers 1..20

FEATURES  
Source

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0193G23"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAAGAA 5411

Db 1 TAAAAAATACAAAAAGAA 20

# RESULT 572

AZ936914

LOCUS 20 bp DNA linear GSS 26-APR-2001

DEFINITION 2M0193G23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION AZ936914

VERSION AZ936914.1 GI:13795495

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0193 row: G column: 23

Seq primer: CACACGAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

1. .20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0193G23"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5412

Db 1 AAAAAATACAAAAAGAA 20

# RESULT 573

AZ949180/c

LOCUS 20 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0212I02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION AZ949180

VERSION AZ949180.1 GI:13820407

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0212 row: I column: 02

Seq primer: CACACGAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

1. .20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC2M0212102"  
/sex="Female"  
/lab\_host="E. coli strain X110-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412  
|||||  
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 574  
LOCUS A2963973 20 bp DNA linear GSS 27-APR-2001  
DEFINITION clone UUGC2M0233J01 F, genomic survey sequence.  
ACCESSION A2963973  
VERSION A2963973.1 GI:13835200  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0233 row: J column: 01  
Seq primer: CGTGTAAACGACGCGCAT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UUGC2M0233J01"  
/sex="Female"  
/lab\_host="E. coli strain X110-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412  
|||||  
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 575  
LOCUS CL680297 20 bp DNA linear GSS 09-JUN-2004  
DEFINITION PRI0128C.G05.2 - PRI0128C.BR (20) Note: Recurring Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL680297  
VERSION CL680297.1 GI:50187127  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
APPABD: an Acedb database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
JOURNAL Contact: Sommer RJ  
COMMENT Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@uebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source 1..20  
Location/Qualifiers  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBp1fos-5 Fosmid vector"

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5406 AAAAAAAAAAATGAAATATA 5425

Db 20 AAAAAAAAAAAGAAAAAAAAA 1

RESULT 576

AL038582

LOCUS AL038582 21 bp mRNA linear EST 06-UTL-2004

DEFINITION DKFZP566P0946.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone

ACCESSION AL038582

VERSION AL038582.1 GI:49682163

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 21)

Ostenweider, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Ostenweider, et al.)

Unpublished (1999)

CONTACT: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.

FEATURES

source

Location/Qualifiers

1..21

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZP566P0946"

/tissue\_type="kidney"

/dev\_stage="fetal"

/lab\_host="X1-2blue"

/clone\_1ib="566 (synonym: hfkcd2)"

/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5402 CAAAAAAAAAATGAAA 5421

Db 2 CAAAAAAAAAATGAAA 21

RESULT 577

AL038839

LOCUS AL038839 21 bp mRNA linear EST 06-UTL-2004

DEFINITION DKFZP566P1346.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone

ACCESSION AL038839

VERSION AL038839.1 GI:49682218

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 21)

Ostenweider, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Ostenweider, et al.)

Unpublished (1999)

CONTACT: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.

FEATURES

source

Location/Qualifiers

1..21

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="DKFZP566P1346"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_1ib="566 (synonym: hfkcd2)"  
/note="Vector: pAMP1, Site\_1: NotI, Site\_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5402 CAAAAAAAAAATGAAA 5421

Db 2 CAAAAAAAAAATGAAA 21

RESULT 578

AL587702/c

LOCUS AL587702 21 bp mRNA linear EST 02-MAR-2001

DEFINITION ROS060H09, mRNA sequence.

ACCESSION AL587702

VERSION AL587702.1 GI:13192736

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 21)

Murray, F.

Unpublished (2001)

CONTACT: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech

(\*6854-

Seq primer: M13P.

FEATURES

source

Location/Qualifiers

1..21

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="ROS060H09"

/tissue\_type="Brain"

/dev\_stage="Unknown"

/lab\_host="DH10B"

/clone\_1ib="BP Chicken Brain Library"

/note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI; Cloned

unidirectionally. Primer: Oligo dt. 5' adaptor sequence:

5' TCGACCTGAG 3', 3' adaptor sequence: 5'

GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from

Clontech (\*6854-1)"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5396 AAAAAAAAAAATGAAAAT 5416

Db 21 AAAAAAAAAAATGAAAAT 1

RESULT 579

BX556006

LOCUS BX556006 21 bp mRNA linear EST 10-OCT-2003

DEFINITION BX556006 Glosina morsitans morsitans adult infected gut Glosina

ACCESSION moritans moritans cDNA clone Tse24c09\_p1c, mRNA sequence.  
 VERSION BX556006  
 KEYWORDS BX556006.1 GI:33379965  
 SOURCE EST.  
 ORGANISM Glossina moritans moritans  
 Glossina moritans moritans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 21)  
 Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*  
*moritans moritans* and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor IL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.  
 FEATURES  
 source Location/Qualifiers  
 1..21  
 /organism="Glossina moritans moritans"  
 /mol\_type="mRNA"  
 /sub\_species="moritans"  
 /db\_xref="taxon:37546"  
 /clone="Tse24c09\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina moritans moritans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.Brucei"

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGGAAA 5412  
 ||||| ||||| ||||| |||||  
 21 AAAAAAAAAAAAAAAAAAAAA 2

Db

RESULT 580  
 EX558161/c 21 bp mRNA linear EST 10-OCT-2003  
 LOCUS BX558161 Glossina moritans moritans adult infected gut Glossina  
 moritans moritans cDNA clone Tse37a05\_p1c, mRNA sequence.  
 ACCESSION BX558161  
 VERSION BX558161.1 GI:33429302  
 KEYWORDS EST.  
 SOURCE Glossina moritans moritans  
 Glossina moritans moritans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 21)  
 Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*  
*moritans moritans* and expression analysis of putative immune  
 response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942

PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor IL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.  
 FEATURES  
 source Location/Qualifiers  
 1..21  
 /organism="Glossina moritans moritans"  
 /mol\_type="mRNA"  
 /sub\_species="moritans"  
 /db\_xref="taxon:37546"  
 /clone="Tse37a05\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina moritans moritans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.Brucei"

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5401 AAAAAAAAAAATGAAA 5420  
 ||||| ||||| ||||| |||||  
 21 AAAAAAAAAAAAAAAAAAAAA 2

Db

RESULT 581  
 CF276638/c 21 bp mRNA linear EST 14-AUG-2003  
 LOCUS CF276638 Oryza sativa (japonica cultivar-group) CDNA clone 14ETL--01-N19,  
 14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) CDNA clone 14ETL--01-N19,  
 mRNA sequence.  
 ACCESSION CF276638  
 VERSION CF276638.1 GI:33654024  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatridae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 FEATURES  
 source Location/Qualifiers  
 1..21  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="14ETL--01-N19"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Rice etiolated leaf plasmid cDNA library  
 (14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412  
|||||  
20 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 582  
CF318152/c 21 bp mRNA linear EST 15-AUG-2003

LOCUS CF318152/c  
DEFINITION ABF--07-G07.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-G07, mRNA sequence.

ACCESSION CF318152 GI:33683675

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL Oryza sativa (japonica cultivar-group)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412  
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20 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 583  
CF318152/c 21 bp mRNA linear EST 15-AUG-2003

LOCUS CF318152/c  
DEFINITION HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-C11, mRNA sequence.

ACCESSION CF318152

VERSION CF318152.1 GI:33689913

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers

1..21  
/organism="Oryza sativa (japonica cultivar-group)"  
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Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412  
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21 AAAAAAAAAAAAAAAAAAAAAA 2

Db

RESULT 584  
CF319122/c 21 bp mRNA linear EST 15-AUG-2003

LOCUS CF319122/c  
DEFINITION HD--09-I07.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-I07, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5406 AAGAGAAAAATCGAATAATAA 5425
Db 21 AACGAAAAAATAATAA 2

RESULT 585
A2346717/c 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0082002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0082002 F, genomic survey sequence.
ACCESSION A2346717
VERSION A2346717.1 GI:10425954
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: O column: 02
Seq primer: CGTGTAAAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0082002"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

```

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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5401 ACAAAAAAGAAAAATGAAA 5420
Db 21 AAAAAAAGAAAGAAAGAAA 2

RESULT 586
A2461824 21 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0267B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0267B23 R, genomic survey sequence.
ACCESSION A2461824
VERSION A2461824.1 GI:10619949
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: B column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

```



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAGAA 5412  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 587  
LOCUS AZ493766 21 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION AZ493766  
VERSION AZ493766.1 GI:10667750  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C., Iselm, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymer Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0328 row: C column: 11  
Seq primer: CACACAGAAACAGCTATAC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source Location/Qualifiers

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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory DNA Resource  
http://www.jax.org/resources/documents/dnares/. The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATCAAAAAGAA 5411  
Db 2 TAAAAAAAAAAAAAAAAA 21

RESULT 588  
LOCUS CL693165 21 bp DNA linear GSS 10-JUL-2004  
DEFINITION PRI0160a.G10.2 - PRI0160a.BR (21) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL693165  
VERSION CL693165.1 GI:50215073  
KEYWORDS GSS.

SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 21)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
Apbads: an Acids database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source Location/Qualifiers

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/clone\_1lb="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBg1fos-5 Fosmid vector"

Query Match 0.3%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5389 AATTAATAATCAAAAAGAA 5408  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 589  
AZ381798/c

LOCUS A2381798 19 bp DNA linear GSS 02-OCT-2000  
 DEFINITION IM0138G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0138G01 R, genomic survey sequence.  
 ACCESSION A2381798  
 VERSION A2381798.1 GI:10495498  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0138 row: G column: 01  
 Seq primer: CACACGAGAAACAGCTATCACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42m; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1270 CCCGACGACGACCA 1284  
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 Db 18 CCCGACGACGACCA 4

RESULT 590  
 AM248747/c  
 LOCUS

AM248747 19 bp mRNA linear EST 07-JAN-2000

DEFINITION 2821119.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.  
 ACCESSION AM248747  
 VERSION AM248747.1 GI:6591740  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other ESTs: 2821119.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgs@bte-remail.nih.gov  
 Tissue Procurement: DCTD/DP CDNA Library Preparation: Ling  
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT) DNA Sequencing by: Berkeley MGC sequencing project  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patchmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 7 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: L1C6M5 row: P column: 16  
 High quality sequence stop: 7.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGA 5410  
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 Db 18 AAAAAATACAAAAGA 1

RESULT 591  
 CF334610/c  
 LOCUS  
 DEFINITION JMT--03-PI3.b1 AtUMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (Japonica cultivar-group) cDNA clone JMT--03-PI3, mRNA sequence.  
 ACCESSION CF334610  
 VERSION CF334610.1 GI:33817556  
 KEYWORDS EST.  
 SOURCE Oryza sativa (Japonica cultivar-group)  
 ORGANISM Oryza sativa (Japonica cultivar-group)

CF334610 19 bp mRNA linear EST 18-AUG-2003  
 JMT--03-PI3.b1 AtUMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (Japonica cultivar-group) cDNA clone JMT--03-PI3, mRNA sequence.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Naim B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnaemg@bio.com, bhnaem@bio.myongji.ac.kr.

FEATURES  
source  
location/Qualifiers

1..19  
/organism="Oryza sativa (japonica cultivar-group)"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ATUMT-overexpressing transgenic rice plasmid cDNA library (UMT)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5398 AATACAAAGAAAAA 5415  
Db 18 AATTAAGAAAAA 1

RESULT 592  
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LOCUS 1M0080H09R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0080H09 R, genomic survey sequence.  
ACCESSION AZ345795  
VERSION AZ345795.1 GI:10425032  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenan,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: H column: 09  
Seq primer: CACACAGAAACGATATACGC  
Class: plasmid ends

FEATURES  
source  
location/Qualifiers

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/db\_xref="taxon:10090"  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5391 TTTAAATATCAAAAA 5408  
Db 1 TTTAAATATCAAAAA 18

RESULT 593  
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LOCUS 1M0360B13F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0360B13 F, genomic survey sequence.  
ACCESSION AZ513919  
VERSION AZ513919.1 GI:10695235  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenan,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
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Unpublished (2000)  
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University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0360 row: B column: 13  
Seq primer: CATTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

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/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
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adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAAATGAAA 5420  
|||||  
18 AAAAAAGAAAAAAA 1

RESULT 594  
AZ650252 19 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0520N17F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0520N17 F, genomic survey sequence.  
ACCESSION AZ650252  
VERSION AZ650252.1 GI:11784550  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Haml,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
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University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0520 row: N column: 17  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5398 AATACAAAGAAAAA 5415  
|||||  
1 AATACAAAGAAAAA 18

RESULT 595  
AZ650575 19 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0520P13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0520P13 R, genomic survey sequence.  
ACCESSION AZ650575  
VERSION AZ650575.1 GI:11785200  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Haml,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0520 row: P column: 13  
Seq primer: CACACAGCAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAA 5408  
 Db 1 TTTAAAAAATACAAAAA 18

RESULT 596  
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 clone UUCG1M0564H19 R, genomic survey sequence.  
 ACCESSION AZ766990  
 VERSION AZ766990.1 GI:12884624  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

TITLE Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,  
 Riedel, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhuesern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

FEATURES  
 source Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0564 row: H column: 19  
 Seg primer: CACACAGGAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19  
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/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAAAATGAAA 5420  
 Db 2 AAAAAAGAAAAAATGAAA 19

RESULT 597  
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 DEFINITION S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
 ACCESSION AM333777  
 VERSION AM333777.1 GI:6830134  
 KEYWORDS EST.

SOURCE Pneumocystis carinii  
 Pneumocystis carinii  
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
 Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 20)  
 Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staden, C.,  
 Edman, J.C., Kovacs, J. and Cushion, M.

TITLE Expressed sequence tags from Pneumocystis carinii  
 Unpublished (2000)  
 Contact: Staden C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY  
 40506-0225, USA

JOURNAL Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staden@pop.uky.edu.  
 Location/Qualifiers  
 1..20  
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 /lab\_host="E. coli"  
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 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
 P. carinii organisms (3x10e6) from a single rat (59-1-6,  
 sacrificed on 3/17/99) at Cincinnati VA facilities.  
 Trizol extracted RNA. Oligo dT priming, standard  
 conditions described by vendor, Stratagene. Further  
 details see www.uky.edu/Project/Pneumocystis/"

**RESULT 599**

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/organism="Homo sapiens"  
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Query Match      0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5391 TTTAAAAAATACAAAAA 5408
Db      3 TTTAAAAAATACAAAAA 20

RESULT 601
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LOCUS      1M0420H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0420H13 R, genomic survey sequence.
ACCESSION      AZ602152
VERSION      AZ602152.1 GI:11724342
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0420 row: H column: 13
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
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/clone="UUGC1M0420H13"
/sex="Male"
/lab.host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

```

```

purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5397 AATACCAAAAGAAAA 5414
Db      20 AATACCAAAATAAAAA 3

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LOCUS      AZ610868
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clone UUGC1M0436G12 F, genomic survey sequence.
ACCESSION      AZ610868
VERSION      AZ610868.1 GI:11733058
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: G column: 12
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Class: plasmid ends
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Location/Qualifiers
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/sex="Male"
/lab.host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to

```





and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATATCAAAAAA 5408  
|||||  
3 TTTAAAAATATCAAAAAA 20

RESULT 605  
CL693164

LOCUS CL693164 21 bp DNA linear GSS 10-JUL-2004  
DEFINITION PRI0160a\_G09\_2 - PRI0160a.BR (21) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL693164  
VERSION CL693164 GI:50215072  
KEYWORDS GSS  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 21)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
JOURNAL Contact: Sommer RJ  
COMMENT Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@uebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Classes: fosmid ends.

FEATURES  
source Location/Qualifiers  
1..21  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBp1fos-5 Fosmid vector"

Query Match 0.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATATCAAAAAA 5410  
|||||  
4 TTTAAAAATATCAAAAAA 21

RESULT 606  
CL693188  
LOCUS CL693188 21 bp DNA linear GSS 10-JUL-2004  
DEFINITION PRI0160c\_F06\_2 - PRI0160c.BR (21) Note: Recurring string Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL693188  
VERSION CL693188 GI:50215096  
KEYWORDS GSS  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
TITLE AppADB: an Acedb database for the nematode satellite organism  
JOURNAL Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@uebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Classes: fosmid ends.

FEATURES  
source Location/Qualifiers  
1..21  
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/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBp1fos-5 Fosmid vector"

Query Match 0.3%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATATCAAAAAA 5410  
|||||  
4 TTTAAAAATATCAAAAAA 21

RESULT 607  
AZ363907  
LOCUS AZ363907/c 19 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0109113R Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0109113 R, genomic survey sequence.

ACCESSION AZ363907  
VERSION AZ363907.1 GI:10477607  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0109 row: 1 column: 13  
Seq primer: CACACAGAAACAGCTATGACC  
Classes: plasmid ends  
High quality sequence stop: 19.  
location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

FEATURES  
source

/clone="UUGC1M0109113"  
/sex="Male"  
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAA 5408  
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 608  
AA954509/c  
LOCUS AA954509 19 bp mRNA linear EST 23-JUN-1998  
DEFINITION on81d05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1563081 3' similar to TR:Q24035 Q24035 ENA POLYPEPTIDE.  
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AA954509  
VERSION AA954509.1 GI:3118204  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
TITLES Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapb-remail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGS Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 754 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES  
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1..19  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1563081"  
/lab\_host="PH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung Nhlh19w, testis NHT, and B-cell NCI-CCGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bernaldo."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3762 GGGCCCCGAGGGCCTGG 3780  
Db 19 GGGGCCCGGGGCTGG 1

RESULT 609  
AJ666205/c  
LOCUS AJ666205 19 bp mRNA linear EST 28-JUN-2004  
DEFINITION AJ666205 CSEORAN09 Sus scrofa cDNA clone C000033\_E15, mRNA sequence.

ACCESSION AJ666205  
VERSION AJ666205.1 GI:49350656  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics

Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross-match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site 1: EcoRI. R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES  
source  
1..19  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C000033\_E15"  
/tissue\_type="Placenta"  
/clone\_lib="CSEORAN09"  
/note="Vector: pBluescriptII (KS+); Site 1: SCOR1; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5399 ATACAAAAAGAAAAATG 5417  
Db 19 AAAAAAAAAAGAAAAAAG 1

RESULT 610  
AJ668179/c  
LOCUS AJ668179 19 bp mRNA linear EST 28-JUN-2004  
DEFINITION AJ668179 CSEORAN09 Sus scrofa cDNA clone C000045\_L19, mRNA sequence.

ACCESSION AJ668179  
VERSION AJ668179.1 GI:49352630  
KEYWORDS EST.

SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mmscore 20 and -mismatch 12 options. Vector:pluScriptII(KS+) R. Site 1:  
 EcorI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute,  
 Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.  
 FEATURES  
 source  
 1. 19  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0000045.1.19"  
 /issue\_type="placenta"  
 /clone\_lib="CSEGRAN09"  
 /note="Vector: pluScriptII(KS+); Site 1: EcorI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."  
 Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3;  
 Oy 5393 AAAAAATACAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 611 19 bp mRNA linear EST 28-JUN-2004  
 AJ669138 CSEGRAN09 Sus scrofa cDNA clone C0000048\_O12, mRNA  
 LOCUS AJ669138  
 DEFINITION Sequence.  
 ACCESSION AJ669138  
 VERSION AJ669138.1 GI:49353592  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mmscore 20 and -mismatch 12 options. Vector:pluScriptII(KS+) R. Site 1:  
 EcorI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute,  
 Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.  
 FEATURES  
 source  
 1. 19  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /mol\_type="mRNA"

/db\_xref="taxon:9823"  
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 /issue\_type="placenta"  
 /clone\_lib="CSEGRAN09"  
 /note="Vector: pluScriptII(KS+); Site 1: EcorI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."  
 Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3;  
 Oy 5393 AAAAAATACAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 612 19 bp mRNA linear EST 06-DEC-2002  
 BQ588729 MP1Z-ADIS-024-storage root Beta vulgaris  
 LOCUS BQ588729  
 DEFINITION CDNA clone 024-014-B24-3-PRIME, mRNA sequence.  
 ACCESSION BQ588729  
 VERSION BQ588729.1 GI:26118312  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelet,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 19 Std Error: 0.00  
 Plate: 14 row: B column: 24  
 Seq primer: T7; GTAATACGACCTCCTATGAGGC.  
 Location/Qualifiers  
 1. 19  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:187281"  
 /clone="024-014-B24"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /lab\_host="EMDH10B"  
 /issue\_type="storage root"  
 /note="Vector: PCMVSPOR6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet. Library provided by KWS Kleinfanzlebener Saatgut AG Eiback, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

	Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	5393	AAAAAATTCAGAAAAAGAA	5411							
Db	1	AAAAAAAAAAAAAAAAAAAAA	19							

RESULT 613				
CB174047/c				
LOCUS	CB174047	19 bp	mRNA	linear EST 09-OCT-2003
DEFINITION	OR 2032F05 010529.y1 Adult mouse olfactory epithelium library Mus musculus cDNA clone 2032F05 5', mRNA sequence.			

ACCESSION	CB174047
VERSION	CB174047.1
KEYWORDS	GI:37592676
SOURCE	EST.
	Mus musculus (house mouse)

ORGANISM  
mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
1 (baes 1 to 19)  
REFERENCE  
Young, J. M., Shykind, B. M., Lane, R. P., Tonnes-Priddy, L., Ross, J. A.,

TITLE	Olfactory receptor expressed sequence tags
JOURNAL	expression of over 400 genes, extensive unequal expression levels
COMMENT	Genome Biol. 4 (11), R71.1-R71.15 (2003) Contact: Young JM

Trask lab, Division of Human Biology  
Fred Hutchinson Cancer Research Center  
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA  
98109-1024, USA  
Tel: 206 667 1471  
Fax: 206 667 6524

**FEATURES**  
 Email: jayoung@fhcrc.org  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. .19  
**SOURCE**

```

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2632F05"
/tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/notes="Organ: Olfactory tubinates; Vector:
lambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Vossahl. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."

```

Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 4e+02;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

QY	5393	AAAAAAAAATACAAAAAAGAA	5411
Db	19	AAAAAAAAAAAAAAAAAAAA	1

RESULT 614	CF279008/c	LOCUS	DEFINITION
	CF279008	19 bp	mRNA
	14ERTL--05-C13.b1	Rice etiolated leaf	plasmid cDNA library (14ERTL)
	Oryza sativa (japonica cultivar-group)	cdna clone	14ERTL--05-C13,
	mRNA sequence.		

ACCESSION	CF279008
VERSION	CF279008.1
	GI:33656394

SOURCE ORGANISM	Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)
-----------------	--

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE	Enhartoidae; Oryzae; Oryza.
AUTHORS	1 (bases 1 to 19)
TITLE	Kim,J.S., Jun,K.M., Cheong,P.-K., Kim,M.J., Lee,T.H., Shin,Y.C.,
JOURNAL	Song,S.-I., Kim,Y.-K., and Naim,B.H.
COMMENT	Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Naim B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**FEATURES**  
**source**

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="cazon:39947"
/clone="14ETL--05-C13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_idb="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 4e+02;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

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QY      5393 AAAAAAAAAATCAAAAAAAAAAGAA 5411
          ||||| | ||||| |
Db      19  AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 615	CF291089/c	LOCUS	DEFINITION
	CF291089	19 bp	mRNA linear
	14RCOT--01-G03.D1	Rice root plasmid	CDNA library (14RCOT) <i>Oryza sativa</i> (japonica cultivar-group) CDNA clone 14RCOT--01-G03, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS

SOURCE	ORGANISM
Oryza sativa (japonica cultivar-group)	
Oryza sativa (japonica cultivar-group)	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	

Spermatophyta; Magnoliophyta;  
Ehrhartoideae; Oryzae; Oryza

REFERENCE	1 (bases 1 to 19)
AUTHORS	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.

TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B. H.

**FEATURES**  
Genomics and Genetics Institute, greenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

**FEATURES**

**SOURCE**

```

"organism="Oryza sativa (japonica cultivar-group)"
"mol_type="rRNA"
"/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="14ROOT--01-G03"
/risuse_type="root"
/dev_stage="14 days after germination"

```

/lab host="E.coli DH10B"  
/clone lib="Rice root plasmid cDNA library (14ROOT)"  
/note=Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411  
19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 616  
CF291090 19 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--01-G03.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA  
sequence.  
ACCESSION CF291090.1 GI:33660123  
VERSION CF291090  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note=Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411  
19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 617  
CF298396/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA  
sequence.  
ACCESSION CF298396  
VERSION CF298396.1 GI:33670157

KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source 1..19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note=Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAAAGAAAAATGAAA 5420  
19 CAAAAAAAAAAAAAAAAAAAA 1

RESULT 618  
CF298472/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-001, mRNA  
sequence.  
ACCESSION CF298472  
VERSION CF298472.1 GI:33670233  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
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QY 5397 AATACAAAAGAGAAAAA 5415  
 19 AATTAATAAAAAAAAAA 1

RESULT 619  
 CF299598 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--03-K23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K23, mRNA  
 sequence.

ACCESSION CF299598 GI:33671359  
 VERSION CF299598  
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
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 /mol\_type="mRNA"  
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 /clone="7LEAF--03-K23"  
 /tissue\_type="leaf"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3;

QY 5393 AAAAAAATACAAAAGAA 5411  
 19 AAAAAAAAAAAAAAAAAA 1

RESULT 620  
 CF300236 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--04-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION

sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L24, mRNA  
 sequence.

ACCESSION CF300236 GI:33671997  
 VERSION CF300236

KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.

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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:39947"  
 /clone="7LEAF--04-L24"  
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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3;

QY 5389 AATTAAAAATACAAA 5407  
 19 AATCAAAAAAAAAAAAAA 1

RESULT 621  
 CF302327 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--07-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L24, mRNA  
 sequence.

ACCESSION CF302327 GI:33674088  
 VERSION CF302327  
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.

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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES

source

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

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/db\_xref="taxon:39947"

/clone="7LEAF--07-L24"

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/issue="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATCAAAAAGAA 5411  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 622  
CF302456/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA  
sequence.  
ACCESSION CF302456  
VERSION CF302456.1 GI:33674217  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--07-P22"

/issue\_type="leaf"

/issue="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5402 CAAAAAAAAATCAAAAAGAA 5420  
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5402 CAAAAAAAAATCAAAAAGAA 5420  
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 623  
CF304589/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS ABP1--05-G10.g1 ABP3-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (ABP1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABP1--05-G10, mRNA sequence.  
ACCESSION CF304589  
VERSION CF304589.1 GI:33676350  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABP1--05-G10"

/issue\_type="leaf"

/issue="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABP3-overexpressing transgenic rice lambda  
phage cDNA library (ABP1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATCAAAAAGAA 5411  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 624  
CF309636/c 19 bp mRNA linear EST 15-AUG-2003  
LOCUS ABP--03-008.g1 ABP3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABP) Oryza sativa (japonica cultivar-group) cDNA clone  
ABP--03-008, mRNA sequence.  
ACCESSION CF309636  
VERSION CF309636.1 GI:33681397  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

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/mol_type="mRNA"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
CDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5390 ATTAATAATACAAAAA 5408  
|||||  
Db 19 ATTCAAAAAAAAAAAAAA 1

## RESULT 625

CF309801/c

## LOCUS

ABF--04-C04.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
ABF--04-C04, mRNA sequence.

## ACCESSION

CF309801

## VERSION

CF309801.1

## KEYWORDS

EST.

## ORGANISM

Oryza sativa (japonica cultivar-group)

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

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/db\_xref="taxon:39947"

/clone="ABF--04-C04"

/tissue\_type="leaf"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid

CDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

element binding transcription factor 3 overexpression

line."

for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411  
|||||  
Db 19 AAAAAAAAAAAAAAAAAA 1

## RESULT 626

CF309943

## LOCUS

ABF--04-F15.b1 ABF3-overexpressing transgenic rice plasmid CDNA  
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
ABF--04-F15, mRNA sequence.

## ACCESSION

CF309943

## VERSION

CF309943.1

## KEYWORDS

EST.

## ORGANISM

Oryza sativa (japonica cultivar-group)

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABF--04-F15"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

CDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411  
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Db 19 AAAAAAAAAAAAAAAAAA 1

## RESULT 627

CF311496

## LOCUS

ABF--06-L18.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
ABF--06-L18, mRNA sequence.



**ACCESSION** CF311496  
**VERSION** CF311496.1 GI:33683257  
**KEYWORDS** EST  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group); Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 19)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--06-M03"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 5393 AAAAAAATGCAGAAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAAAAAA 1

**RESULT** 628  
**CF311513** 19 bp mRNA linear EST 15-AUG-2003  
**LOCUS** ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid CDNA  
**DEFINITION** library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--06-M03, mRNA sequence.  
**ACCESSION** CF311513  
**VERSION** CF311513.1 GI:33683274  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group); Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 19)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**FEATURES**  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 5393 AAAAAAATGCAGAAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAAAAAA 1

**RESULT** 629  
**CF312403** 19 bp mRNA linear EST 15-AUG-2003  
**LOCUS** ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid CDNA  
**DEFINITION** library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--08-C07, mRNA sequence.  
**ACCESSION** CF312403  
**VERSION** CF312403.1 GI:33684164  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group); Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 19)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAA 5411  
 |||||  
 1 AAAAAAAAAAAAAAAAAA 19

RESULT 630  
 CF315299/C  
 LOCUS CF315299/C  
 DEFINITION HD--04-C17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--04-C17, mRNA sequence.

ACCESSION CF315299  
 VERSION CF315299  
 KEYWORDS  
 SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, U. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /clone="HD--04-C17"  
 /tissue\_type="callus"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAA 1

RESULT 631  
 CF316480  
 LOCUS CF316480/C  
 DEFINITION HD--05-M14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-M14, mRNA sequence.

ACCESSION CF316480  
 VERSION CF316480  
 KEYWORDS  
 SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
 1 (bases 1 to 19)  
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,  
 Song, S. I., Kim, U. K., Kim, Y. -K. and Nahm, B. H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

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 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 19  
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 /tissue\_type="callus"  
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 /clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAA 5411  
 |||||  
 19 AAAAAAAAAAAAAAAAAA 1

RESULT 632  
 CF318788  
 LOCUS CF318788  
 DEFINITION HD--09-A23.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-A23, mRNA sequence.

ACCESSION CF318788  
 VERSION CF318788  
 KEYWORDS  
 SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, U. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

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Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:39947"  
 /clone="HD--09-A23"

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/cisue_type="callus"
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/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411
|||||
1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 633
CF329136/c 19 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION NACL--04-F15.b1 Rice callus plasmid cDNA clone NACL--04-F15, mRNA
sequence.
ACCESSION CF329136
VERSION CF329136.1 GI:33806509
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
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/cisue_type="callus"
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/lab_host="R.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5397 AAAAAATACAAAAAGAA 5415
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19 AAAAAAAGAAAAAAAAAAAA 1

RESULT 634
CF329137 19 bp mRNA linear EST 18-AUG-2003
LOCUS CF329137
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DEFINITION NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
sequence.
ACCESSION CF329137
VERSION CF329137.1 GI:33806511
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="R.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAA 5413
|||||
1 AAAAAATAAAAAAAAAAAA 19

RESULT 635
CF329986 19 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-109.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION NACL--05-109.b1 Rice callus plasmid cDNA clone NACL--05-109, mRNA
sequence.
ACCESSION CF329986
VERSION CF329986.1 GI:33808194
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
```



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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_1lb="JMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAA 5411

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 639  
LOCUS CF334014/c 19 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--03-C09.g1 AcJMT-overexpressing transgenic rice plasmid CDNA library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone JMT--03-C09, mRNA sequence.

ACCESSION CF334014.1 GI:33816333

VERSION

KEYWORDS

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
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Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

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1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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CDNA library (JMT)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
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methyltransferase overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 640  
LOCUS CNS45602/c 19 bp mRNA linear EST 30-APR-2004  
DEFINITION EST 17546 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA clone B3CS00RL003H10 3', mRNA sequence.

ACCESSION CNS45602.1 GI:46910227

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera  
Vitis vinifera  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 19)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UMR 619 - Equipe Biologie de la Vigne  
Universite de Bordeaux I, Institut National de la Recherche  
Agronomique  
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,  
France  
Tel: 00-33-(0)5-57-12-25-50  
Fax: 00-33-(0)5-57-12-25-48  
Email: s.hamdi@bordeaux.inra.fr  
Seq primer: 77.

# FEATURES

source

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1. 19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
StiIa; Site_2: StiIb; Oriented library"
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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 641  
LOCUS CNS45922/c 19 bp mRNA linear EST 30-APR-2004  
DEFINITION EST 17866 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA clone B3CS00RL006D07 3', mRNA sequence.

ACCESSION CNS45922.1 GI:46910547

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera  
Vitis vinifera  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; Vitaceae; Vitis.

1 (bases 1 to 19)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,  
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,  
Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp  
or seeds) at Various Developmental Stages

Unpublished (2002)

JOURNAL  
COMMENT

Contact: Hamdi S.

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Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

## FEATURES

source

Location/Qualifiers

1..19

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="B3CS00RL006D07"

/dev\_stage="ripening stage"

/clone\_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:

SflIA; Site\_2: SflIB; Oriented library"

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 642

CNS45964/c

LOCUS

DEFINITION EST 17912 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

ACCESSION

CNS45964

VERSION

CNS45964.1

KEYWORDS

EST.

SOURCE

ORGANISM

Vitis vinifera

Vitis vinifera

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 19)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

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Unpublished (2002)

Contact: Hamdi S.

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Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..19

/organism="Vitis vinifera"

/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
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/dev\_stage="ripening stage"  
/clone\_lib="Ripe Grape Skin Triplex2 Library"  
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site\_1:  
SflIA; Site\_2: SflIB; Oriented library"

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 643

CNS46303/c

LOCUS

DEFINITION EST 18255 Green Grape Berry Lambda Triplex2 Library Vitis vinifera

cDNA clone B3CS1XGB015R10 3', mRNA sequence.

ACCESSION

CNS46303

VERSION

CNS46303.1

KEYWORDS

EST.

SOURCE

ORGANISM

Vitis vinifera

Vitis vinifera

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 19)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..19

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clone="B3CS1XGB015R10"

/dev\_stage="green stage"

/clone\_lib="Green Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site\_1: SflIA; Site\_2: SflIB; Oriented library"

QY 5393 AAAAAAAAAACAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 644

AZ307313

LOCUS

DEFINITION IM0008H20R Mouse 10kb plasmid U06C1M library Mus musculus genomic

clone UUGC1M0008H20 R, genomic survey sequence.

ACCESSION AZ307313 GI:10346192

VERSION AZ307313.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0008 row: H column: 20  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends

FEATURES

source High quality sequence stop: 19.

Location/Qualifiers

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/db\_xref="taxon:10090"

/clone="UUGC1M0008H20"

/sex="Male"

/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1lb="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 19

Db

RESULT 645  
AZ310079 19 bp DNA 1linear GSS 29-SEP-2000  
LOCUS IM0018K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0018K17 R, genomic survey sequence.

AZ310079

ACCESSION AZ310079 GI:10351709

VERSION AZ310079.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0018 row: K column: 17  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends

FEATURES

source High quality sequence stop: 19.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0018K17"

/sex="Male"

/lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1lb="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411  
|||||  
19 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 646  
AZ310105 19 bp DNA 1linear GSS 29-SEP-2000  
LOCUS IM0018E21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0018E21 R, genomic survey sequence.

VERSION	AZ310105.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Bascorn,T., Duval,B., Hamil,C., Jellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedersachsen,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
TITLE	Contract: Robert B. Weiss
JOURNAL	University of Utah
COMMENT	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0018 row: B column: 21 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19
FEATURES	
source	

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0018R21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 [gi|47321414|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

	Query Match	Similarity	Score	DB	Length
Best Local	84.2%	Pred. No.	4e+02	3;	Gaps 0
Matches	16;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0
Oy	5393	AAAAAAAAATCAAAAAAGAA	5411		
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1		

RESULT	647
AZ317743	
LOCUS	
DEFINITION	19 bp DNA linear GSS 29-SEP-2000
ACCESSION	AZ317743
VERSION	AZ317743.1 GI:10366848
	clone UUGC1M0036B18 R, genomic survey sequence.

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi; Eumarkaria; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 19) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D. Weis, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weis University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0036 row: B column: 18 Seq primer: CACACAGAAACAGACTTGAC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. .19
FEATURES	
source	

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/clone="UUGCM0036B18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1fb="Mouse 10kb plasmid UUGCM1 library"  
/note="Vector: PWD242; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

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Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGA 5411
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db 1 AAAAAAAAAAAAAAAAAAAAAA 19

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RESULT	648				
LOCUS	A2340311/C				
DEFINITION	A2340311	19 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0072H15F	Mouse 10kb	plasmid	UUCGIM	library Mus musculus genomic
DEFINITION	clone UUCGIM0072H15 F,	genomic	survey	sequence.	
ACCESSION	A2340311				
VERSION	A2340311.1				GI:10415441
KEYWORDS	GSS.				



SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Relly,M., Rose,M., Rose,R., Stokes,R., Tinger,A., von Niederhausern,A. and Wright,D.,Weiss,R.
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0072 row: H column: 15 Seq primer: CGTTGTAAACGACGCGCAGT Class: plasmid end High quality sequence stop: 19. Location/Qualifiers 1..19
FEATURES	
source	

1. 19  
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/mol\_type="genomic DNA"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1fb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42ny; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g14732114[9b]/R129072.11), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

	Query Match	0.3%	Score 14.2	DB 1	Length 19
	Best Local Similarity	84.2%	Pred. No. 4e+02		
	Matches 16	Conservative 0	Mismatches 3	Indels 0	Gaps 0
OY	5393 AAAAAATACAAAAGAA	5411			
Dd	19 AAAAAAAAAAAAAAAAAA	1			

RESULT	649
AZ345499/c	
LOCUS	
DEFINITION	AZ345499 19 bp DNA linear GSS 29-GRP-2000
clone UGTC1M0806 F, genomic survey sequence.	
ACCESSION	
VERSION	AZ345499.1 GI:10424736
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)

ORGANISM      Mus musculus  
Butariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE      1 (bases 1 to 19)  
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Isaiah, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellay, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb  
                 plasmid inserts  
JOURNAL      Unpublished (2000)  
COMMENT      Contact: Robert B. Weiss  
                 University of Utah Genome Center  
                 University of Utah  
                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
                 84112, USA  
                 Tel.: 801 585 5606  
                 Fax: 801 585 7177  
                 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
                 Insert Length: 10000    Std Error: 0.00  
                 Plate: 0080    row: P    column: 06  
                 Seq primer: CATTGTAAACGACGCGCAGT  
                 Class: plasmid ends  
                 High quality sequence stop: 19.  
                 location/Qualifiers  
SOURCE      1. .19

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 /note="Vector: PMD42ny, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (http://4732114|9d|AF12072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."`

Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 4e+02;		
Matches	16;	Conservative	0;	Mismatches 3; Indels 0
QY	5396	AAATATCAAAAAGAAAA	5414	
DB	19	AAAAAAAAAAGAAAAA	1	

RESULT	650
AZ350519/c	
LOCUS	AZ350519
DEFINITION	19 bp DNA linear
ACCESSION	U0088A10 Mouse 10kb plasmid; UGCIM library Mus musculus genomic clone U0088A10 F, genomic survey sequence.
VERSION	AZ350519
KEYWORDS	AZ350519.1 GI:10429756
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0088 row: A column: 10  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
location/Qualifiers  
1..19  
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/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5393 AAAAAATCAAAAAAGAA 5411  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 651  
AZ364226  
LOCUS AZ364226 19 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0110524F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M0110524 F, genomic survey sequence.  
ACCESSION AZ364226  
VERSION AZ364226.1 GI:10477926  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rellly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0110 row: B column: 24  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
location/Qualifiers  
1..19  
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/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 1 AAAAAAAAAAAAAAAAAA 19

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clone UUCG1M0112A07 R, genomic survey sequence.  
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SOURCE Mus musculus (house mouse)  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islem,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0112 row: A column: 07  
 Seq primer: CACACAGAAACGCTATGAC  
 Class: plasmid ends  
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 /clone\_1lb="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAATCAAAAAAGAA 5411  
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RESULT 653  
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 clone UUC1M0127D10 F, genomic survey sequence.  
 ACCESSION AZ374409  
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 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islem,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
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 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0127 row: D column: 10  
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 High quality sequence stop: 19.  
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 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAATCAAAAAAGAA 5411  
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 1 AAAAAAAAAAAAAAAAAAAAAA 19  
 Db

RESULT 654  
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 clone UUC1M0127F04 R, genomic survey sequence.  
 ACCESSION AZ374619  
 VERSION AZ374619.1 GI:10488119  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0127 row: F column: 04  
 Seq primer: CACACAGGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 655  
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 DEFINITION 1M014410R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M014410 R, genomic survey sequence.  
 ACCESSION A2385952  
 VERSION A2385952.1 GI:10499652  
 KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0144 row: L column: 10  
 Seq primer: CACACAGGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source Location/Qualifiers

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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411  
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 656  
 A2391509  
 LOCUS A2391509 19 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0153K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0153K08 R, genomic survey sequence.  
 ACCESSION A2391509  
 VERSION A2391509.1 GI:10506552  
 KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE  
Niederhausern, A. and Wright, D., Weis, R.  
JOURNAL  
Mouse whole genome scaffolding with paired end reads from 10kb  
COMMENT  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0153 row: K column: 08  
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Class: plasmid ends  
High quality sequence stop: 19.  
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/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411  
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1 AAAAAAAAAAAAAAAAAAAAAA 19

Db

RESULT 657  
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LOCUS  
DEFINITION  
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clone UUCG1M0182P04 F, genomic survey sequence.  
ACCESSION  
AZ410050  
VERSION  
AZ410050.1 GI:10534063  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL  
Plasmid inserts  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0182 row: P column: 04  
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High quality sequence stop: 19.  
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/lab\_host="B. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411  
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1 AAAAAAAAAAAAAAAAAAAAAA 19

Db

RESULT 658  
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LOCUS  
DEFINITION  
1M018013R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
clone UUCG1M018013 R, genomic survey sequence.  
ACCESSION  
AZ414413  
VERSION  
AZ414413.1 GI:10538426  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT

Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0188 row: 0 column: 13  
Seq primer: CACACAGAAACAGCTATCACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No.4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

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LOCUS A2422604  
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clone UUC1M0201B21 F, genomic survey sequence.  
ACCESSION A2422604  
VERSION A2422604.1 GI:10546617  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0201 row: B column: 21  
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High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
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/mol\_type="genomic DNA"  
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No.4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAA 5411  
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1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 660  
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LOCUS A2424716  
DEFINITION 1M0204020F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0204020 F, genomic survey sequence.  
ACCESSION A2424716  
VERSION A2424716.1 GI:10546729  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0204 row: 0 column: 20  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

## FEATURES

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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUC1M0204020"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 661  
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DEFINITION 1M02333D01F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0233D01 F, genomic survey sequence.  
ACCESSION AZ441329  
VERSION AZ441329.1 GI:10565342  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0233 row: 0 column: 01  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

## FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0233D01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 662  
AZ442365/c 19 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0236C13F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0236C13 F, genomic survey sequence.  
ACCESSION AZ442365  
VERSION AZ442365.1 GI:10565378  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0236 row: C column: 13  
Seq primer: CGTGTGAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

**Source**

Query Match	0.3%	Score 14.2	DB 1	Length 19
Best Local Similarity	84.2%	Pred. No. 4e+02		
Matches	16	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
Qy	5393	AAAAAAAAATGCAAAAAAGAA	5411	
db	19	AAAAAAAAAAAAAAAAAAAAA	1	

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Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0255 row: G column: 11.  
Seq primer: CACACAGGAACGCTATGACC  
Class: plaemid ends  
High quality sequence stop: 19.

## FEATURES

**Source**

Query Match	0.3%	Score 14.2	DB 1	length 19
Best Local Similarity	84.2%	Pred. No. 4e+02		
Matches	16	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
Qy	5393	AAAAAAAAATACAAAAAGCA	5411	
Db	19	AAAAAAAAAAAAAAAAAAAA	1	

**JOURNAL COMMENT**  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah

**COMMENT**

Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT



84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0266 Row: B Column: 03  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0266R03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAGAA 5411  
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 665  
 AZ471494/c 19 bp DNA linear GSS 04-OCT-2000  
 LOCUS IM0286E11F Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 DEFINITION clone UGGCM0286E11 F, genomic survey sequence.  
 ACCESSION AZ471494  
 VERSION AZ471494.1 GI:10629619  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weis, R.  
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 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 JOURNAL University of Utah Genome Center  
 COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0266 Row: B Column: 11  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGCM0266R11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UGGCM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5393 AAAAAAAAAACAAAAGAA 5411  
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 666  
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 LOCUS IM0295F04R Mouse 10kb plasmid UGGCM library Mus musculus genomic  
 DEFINITION clone UGGCM0295F04 R, genomic survey sequence.  
 ACCESSION AZ476576  
 VERSION AZ476576.1 GI:10634701  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weis, R.  
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 CONTACT: Robert B. Weiss  
 JOURNAL University of Utah Genome Center  
 COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0295 row: F column: 04  
Seq primer: CACACAGGAAACGCTATACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG1M0295F04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411  
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 667  
LOCUS AZ486786 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0315D21P Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0315D21 F, genomic survey sequence.  
ACCESSION AZ486786  
VERSION AZ486786.1 GI:10653902  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: D column: 21  
Seq primer: CATTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_11b="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411  
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 668  
LOCUS AZ490652 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0323B17R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0323B17 R, genomic survey sequence.  
ACCESSION AZ490652  
VERSION AZ490652.1 GI:10661595  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

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plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

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University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0323 row: E column: 17  
 Seq primer: CACACAGGAAACGCTATACAC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

Plate: 0350 row: B column: 04  
 Seq primer: CGTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0350B04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
 Best Local Similarity 84.2%; Score 14.2; DB 1; Length 19;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match  
 Best Local Similarity 84.2%; Score 14.2; DB 1; Length 19;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAA 5411  
 Db 19 AAAAAAAAAAAGAA 1

Qy 5393 AAAAAAAAAAAGAA 5411  
 Db 1 AAAAAAAAAAAGAA 19

RESULT 669  
 AZ508040 19 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0350804F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0350804 F, genomic survey sequence.  
 ACCESSION AZ508040  
 VERSION AZ508040.1 GI:10689356  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

RESULT 670  
 AZ509929 19 bp DNA linear GSS 05-OCT-2000  
 LOCUS 1M0354A07F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0354A07 F, genomic survey sequence.  
 ACCESSION AZ509929  
 VERSION AZ509929.1 GI:10691245  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0354 row: A column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

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/db\_xref="taxon:10090"  
/clone="U06C1M0354A07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5401 ACAAAGAAAGAAATGAA 5419  
|||||

Db 1 AAAAAAAAAAAAAATTAA 19

## RESULT 671

AZ579119

LOCUS 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0363M16F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C1M0363M16 F, genomic survey sequence.

ACCESSION

AZ579119

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0363 row: M column: 16  
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAA 5411  
|||||

Db 1 AAAAAAAAAAAAAAAA 19

## RESULT 672

AZ583970

LOCUS 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0388M1F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C1M0388M1 F, genomic survey sequence.

ACCESSION

AZ583970

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0388 row: M column: 11  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends

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High quality sequence stop: 19.  
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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5393 AAAAAAAAAACAAAGAA 5411  
1 AAAAAAAAAAAAAAAAAA 19  
Db

RESULT 673  
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LOCUS 1M0391D21F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION Clone UUC1M0391D21 F, genomic survey sequence.  
ACCESSION A2585865  
VERSION A2585865.1 GI:11708055  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B., R.  
Niederhausern,A. and Wright,D., Weis,B., R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0391 row: D column: 21  
Seq primer: CGTTCTAAACGACGCCAGCT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0391D21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5393 AAAAAAAAAACAAAGAA 5411  
1 AAAAAAAAAAAAAAAAAA 19  
Db

RESULT 674  
A2593210 19 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0404C09R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION Clone UUC1M0404C09 R, genomic survey sequence.  
ACCESSION A2593210  
VERSION A2593210.1 GI:11715400  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B., R.  
Niederhausern,A. and Wright,D., Weis,B., R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0404 row: C column: 09  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

source

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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411  
|||||  
1 AAAAAAAAAAAAAAAAAA 19

Db

RESULT 675  
A2616154/C 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0445P16R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0445P16 R, genomic survey sequence.  
ACCESSION A2616154  
VERSION A2616154.1 GI:11738344  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0445 row: P column: 16  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19

FEATURES  
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/organism="Mus musculus"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match  
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411  
|||||  
1 AAAAAAAAAAAAAAAAAA 19

Db

RESULT 676  
A2627844/C 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0474J05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0474J05 F, genomic survey sequence.  
ACCESSION A2627844  
VERSION A2627844.1 GI:11750130  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: J column: 05  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19

FEATURES  
source

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gbl|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 678  
A2631701 19 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0486E01F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M0486E01 F, genomic survey sequence.  
ACCESSION A2631701  
VERSION A2631701.1 GI:11753891  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0486 row: E column: 01  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

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/strain="C57BL/6J"  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gbl|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 678  
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LOCUS 1M0489H15F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC1M0489H15 F, genomic survey sequence.  
ACCESSION A2633821  
VERSION A2633821.1 GI:11756011  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: H column: 15  
Seq primer: CGTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

#### FEATURES

source 1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUC1M0489H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 679  
AZ643659  
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DEFINITION IM0507D18F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0507D18 F, genomic survey sequence.  
ACCESSION AZ643659  
VERSION AZ643659.1 GI:11771446  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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High quality sequence stop: 19.  
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 680  
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LOCUS 19 bp DNA linear GSS 14-DEC-2000  
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clone UUC1M0508E17 R, genomic survey sequence.  
ACCESSION AZ644698  
VERSION AZ644698.1 GI:11773485  
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SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XU10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
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QY 5393 AAAAAAAAAATCAAGAA 5411  
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 Db 19 AAAAAAAAAAAAAAAAAA 1

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 DEFINITION clone UUC1M0511G04 R, genomic survey sequence.  
 ACCESSION AZ645841  
 VERSION AZ645841.1 GI:11775726  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
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 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 High quality sequence stop: 19.  
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XU10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
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QY 5407 AAGAAAAATGAAATTA 5425  
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 Db 19 AAAAAAAAAAGAAAAAAAAA 1

RESULT 682  
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 LOCUS 1M0517L16F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 DEFINITION clone UUC1M0517L16 F, genomic survey sequence.  
 ACCESSION AZ648335  
 VERSION AZ648335.1 GI:11780699  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.  
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 JOURNAL Unpublished (2000)  
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 University of Utah Genome Center  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411  
DB 1 AAAAAAAAAAAAAAAAAA 19

RESULT 683  
LOCUS A2649888 19 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0519E15R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0519E15 R, genomic survey sequence.  
ACCESSION A2649888  
VERSION A2649888.1 GI:11783820  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Nederhausern, A. and Wright, D., Weiss, R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 684  
LOCUS A2764497 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0560H03R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0560H03 R, genomic survey sequence.  
ACCESSION A2764497  
VERSION A2764497.1 GI:12879521  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Nederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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High quality sequence stop: 19.  
Location/Qualifiers

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/sex="Male"  
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/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gbl|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAA 19

## RESULT 685

A2764522

LOCUS

DEFINITION 19 bp DNA linear GSS 16-FEB-2001

clone UUCG1M0560E16 R, genomic survey sequence.

ACCESSION

A2764522

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS

MUSCULUS

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

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/organism="Mus musculus"

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/clone\_lib="Mouse 10kb plasmid UUCG1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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Unpublished (2000)  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
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/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gbl|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAA 19

## RESULT 686

A2764534

LOCUS

DEFINITION 19 bp DNA linear GSS 16-FEB-2001

clone UUCG1M0560P14 R, genomic survey sequence.

ACCESSION

A2764534

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS

MUSCULUS

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

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/organism="Mus musculus"

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/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
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Unpublished (2000)  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411  
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Db 1 AAAAAAAAAAAAAAAAAA 19

# RESULT 687

AZ770387

LOCUS A2770387 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 1M0571123R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0571123 R, genomic survey sequence.

ACCESSION A2770387  
VERSION A2770387.1 GI:12891520

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0571 row: L column: 23

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Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

source

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

# RESULT 688

AZ775624

LOCUS A2775624 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M008E01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCG2M008E01 R, genomic survey sequence.

ACCESSION A2775624  
VERSION A2775624.1 GI:12902356

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

Contact: Robert B. Weiss  
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University of Utah

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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: E column: 01

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

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/clone\_lib="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5397 AATTCACCAAAAGAAAA 5415  
Db 1 ACACACCAAAAGAAAAA 19

RESULT 689  
LOCUS A2778658 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0014020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0014020 F, genomic survey sequence.

ACCESSION A2778658  
VERSION A2778658.1 GI:12908925  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0014 row: 0 column: 20  
Seq primer: CGTGTAAACGACGCCACGT

Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source Location/Qualifiers  
1..19

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACCAAAAGAA 5411  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 690  
LOCUS A2779901 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0016161R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M001616 R, genomic survey sequence.

ACCESSION A2779901  
VERSION A2779901.1 GI:12911024  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis  
University of Utah Genome Center

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Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: E column: 16  
Seq primer: CACACAGCAACACGTATGACC

Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source Location/Qualifiers  
1..19

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
1 AAAAAAAAAAAAAAAAAAAAAA 19  
Db

RESULT 691  
LOCUS A2781876 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0021003 R, genomic survey sequence.  
ACCESSION A2781876  
VERSION A2781876.1 GI:12915007  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT University of Utah Genome Center  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0021 row: 0 column: 03  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
location/Qualifiers

1. 19

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
1 AAAAAAAAAAAAAAAAAAAAAA 19  
Db

RESULT 692  
LOCUS A2786336/c 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0031H17 R, genomic survey sequence.  
ACCESSION A2786336  
VERSION A2786336.1 GI:12923992  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT University of Utah Genome Center  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: H column: 17  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
location/Qualifiers

1. 19

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5396 AAAATACAAAAAGAAAA 5414  
Db 19 AAAAAAAAAAGAAAAA 1

RESULT 693  
AZ787634/c 19 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0034M12 F, genomic survey sequence.

ACCESSION AZ787634  
VERSION AZ787634.1 GI:12926621  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: M column: 12  
Seq primer: CATTCTAAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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/organism="Mus musculus"  
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/clone="UUGC2M0034M12"  
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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 694  
AZ788058/c 19 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0034I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0034I24 R, genomic survey sequence.

ACCESSION AZ788058  
VERSION AZ788058.1 GI:12927475  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: I column: 24  
Seq primer: CACACAGAAACAGCTATGAC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAATACAAAAGAA 5411  
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19 AAAAAAAAAAAAAAAAAA 1

RESULT 695  
LOCUS AZ789590/c 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0037G06R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCG2M0037G06 R, genomic survey sequence.  
ACCESSION AZ789590  
VERSION AZ789590.1 GI:12930573  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0037 row: G column: 06  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
SOURCE Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone="UGCG2M0037G06"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

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Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAATACAAAAGAA 5411  
|||||  
19 AAAAAAAAAAAAAAAAAA 1

RESULT 696  
LOCUS AZ792713/c 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0045C22F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCG2M0045C22 F, genomic survey sequence.  
ACCESSION AZ792713  
VERSION AZ792713.1 GI:12936930  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: C column: 22  
Seq primer: CGTTGTAAACGACGCCACAGT  
Class: plasmid ends  
High quality sequence stop: 19.

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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UGCG2M0045C22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."



inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAGAA 5411  
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19 AAAAAAAAAAAAAAAAAA 1

RESULT 697  
AZ795403 19 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0049C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0049C12 R, genomic survey sequence.

ACCESSION AZ795403  
VERSION AZ795403.1 GI:12942392

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
1 (bases 1 to 19)  
Irelam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0049 row: C column: 12  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0049C12"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb]|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAGAA 5411  
|||||  
19 AAAAAAAAAAAAAAAAAA 1

RESULT 698  
AZ801970 19 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0060112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0060112 R, genomic survey sequence.

ACCESSION AZ801970  
VERSION AZ801970.1 GI:12954293

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
1 (bases 1 to 19)  
Irelam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0060 row: I column: 12  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

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source Location/Qualifiers

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0060112"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114[gb]|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 699  
AZ822225 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0139G08R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCG2M0139G08 R, genomic survey sequence.

ACCESSION AZ822225  
VERSION AZ822225.1 GI:12992133  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0095 row: E column: 17  
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/clone="UGCG2M0139G08"

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/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g1|473214|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 700  
AZ841581 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0139G08R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCG2M0139G08 R, genomic survey sequence.

ACCESSION AZ841581  
VERSION AZ841581.1 GI:13011489  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0139 row: G column: 08  
Seq primer: CACACAGAAACACGTATGAC

Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/organism="Mus musculus"  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0139G08"

1..19  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g1|473214|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAA 5411  
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Db 1 AAAAAAAAAAAAAAAAAA 19

## RESULT 701

AZ841622

LOCUS 19 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0139A16 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0139A16 R, genomic survey sequence.  
AZ841622

VERSION  
KEYWORDS  
SOURCE GSS.  
GI:13011530

ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT Contact: Robert B. Weiss  
University of Utah  
Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0139 row: A column: 16  
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMDA2 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAA 5411  
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Db 1 AAAAAAAAAAAAAAAAAA 19

## RESULT 702

AZ861896

LOCUS 19 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0168P10 R, genomic survey sequence.  
AZ861896

VERSION  
KEYWORDS  
SOURCE GSS.  
GI:13058674

ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT Contact: Robert B. Weiss  
University of Utah  
Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0168 row: P column: 10  
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0168P10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMDA2 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; Mismatches 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 703  
A2936798 19 bp DNA linear GSS 26-APR-2001  
LOCUS 2M0193L10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0193L10 R, genomic survey sequence.  
ACCESSION A2936798  
VERSION A2936798.1 GI:13795379  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
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Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0193 row: L column: 10  
Seq primer: CACACAGAAAACGCTATGACG  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UUGC2M0193L10"  
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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (g1[473214|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4e+02; Mismatches 3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411  
|||||  
1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 704  
A2962226 19 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0231A02 F, genomic survey sequence.  
ACCESSION A2962226  
VERSION A2962226.1 GI:13833453  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0231 row: A column: 02  
Seq primer: CGTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source 1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0231A02"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (g1[473214|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Best Local Similarity 84.2%; Pred. No. 4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAAAGAA 5412  
 Db 1 AAAAAAAAAAAGAA 19

## RESULT 705

A2985501

LOCUS 19 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0267E21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0267E21 F, genomic survey sequence.

ACCESSION

A2985501

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0267 row: E column: 21

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0267E21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g14732114[gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAA 5411  
 Db 1 AAAAAAAAAAAGAA 19

## RESULT 706

BH000498

LOCUS 19 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0288I21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0288I21 F, genomic survey sequence.

ACCESSION

BH000498

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weis  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: I column: 21

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0288I21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g14732114[gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	5393	AAAAAATACAAAAACA	5411	
LOCUS	19 bp	DNA	linear	GSS 15-JAN-2004
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, right border, clone 515E07, genomic survey sequence.			
ACCESSION	AU600883			
VERSION	AU600883			
KEYWORDS	GSS: right border; T-DNA flanking sequence.			
ORGANISM	Arabidopsis thaliana (thale cress)			
REFERENCE	1 Brunaud, V., Balergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Dekose, R., Pelletier, G., Lepoint, B., Caboche, M., and Lecharny, A. T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)			
JOURNAL	22363535			
MEDLINE	12446565			
REFERENCE	2 (bases 1 to 19)			
AUTHORS	Balergue, S.			
JOURNAL	Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE			
COMMENT	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiolegen.fr">http://genoplante-info.infobiolegen.fr</a> ).			
FEATURES	location/Qualifiers			
SOURCE	1..19			
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	/mol_type="genomic DNA"			
	/cultivar="Wassilewskija"			
	/db_xref="taxon:3702"			
	/clone="515E07"			
	/clone_lib="Arabidopsis thaliana T-DNA insertion lines"			
	1..19			
	/note="T-DNA flanking sequence			
	right border"			
misc_feature				
Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4e+02;	3;	Indels 0;
Matches	16;	Conservative 0;	Mismatches 3;	Gaps 0;
QY	5405	AAAAAATAATGAAAAATA	5423	
Db	19	AAAAAATAATGAAAAATA	1	
RESULT 708				
LOCUS	19 bp	DNA	linear	GSS 09-JUL-2004
DEFINITION	PR1012a HO7 2 - PR1012a.BR (19) Note: Recurring String Mixed stage foemid2 libray of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.			
ACCESSION	CL680736			
VERSION	CL680736			
	GI:50187696			

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KEYWORDS      GSS.
SOURCE        Pristionchus pacificus
ORGANISM      Pristionchus pacificus
              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
              Neodiplogasteridae; Pristionchus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE         AppaDb: an AcdeB database for the nematode satellite organism
              Pristionchus pacificus
JOURNAL       Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT       Contact: Sommer RJ
              Evolutionary Biology
              Max-Planck-Institute for Developmental Biology
              Spemannstr. 37-39, Tuebingen D-72076, Germany
              Tel: 00497071601371
              Fax: 00497071601498
              Email: raf.f.sommer@cuebingen.mpg.de
              This library was generated at Caltech, Pasadena, USA and end
              sequenced at Vancouver, Canada.
              Seq primer: T7
              Class: fosmid ends.

FEATURES
  source
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      1..19
        /organism="Pristionchus pacificus"
        /mol_type="genomic DNA"
        /strain="California"
        /db_xref="taxon:54126"
        /clone_lib="Mixed stage fosmid library of P. pacificus
        var. California"
        /note="Vector: pBpicfos-5 Fosmid vector"

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Beet Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY      5393 AAAAAAAAAACCAAAAGCA 5411
Db      1 AAAAAAAAAAAAAAAAAA 19

RESULT 709
CL685439      19 bp      DNA      linear      GSS 09-JUL-2004
LOCUS        PRI0141b.A04.2 - PRI0141b.BR (19) Mixed stage fosmid library of P.
DEFINITION   pacificus var. California Pristionchus pacificus genomic, genomic
              survey sequence.
ACCESSION    CL685439
VERSION      CL685439.1 GI:50193696
KEYWORDS     GSS.
SOURCE       Pristionchus pacificus
ORGANISM     Pristionchus pacificus
              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
              Neodiplogasteridae; Pristionchus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE         AppaDb: an AcdeB database for the nematode satellite organism
              Pristionchus pacificus
JOURNAL       Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT       Contact: Sommer RJ
              Evolutionary Biology
              Max-Planck-Institute for Developmental Biology
              Spemannstr. 37-39, Tuebingen D-72076, Germany
              Tel: 00497071601371
              Fax: 00497071601498
              Email: raf.f.sommer@cuebingen.mpg.de
              This library was generated at Caltech, Pasadena, USA and end
              sequenced at Vancouver, Canada.
              Seq primer: T7
              Class: fosmid ends.

FEATURES
  source
    location/Qualifiers
      1..19
        /organism="Pristionchus pacificus"
        /mol_type="genomic DNA"

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Query Match          0.3% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY      5393 AAAAAAAAAACAAAGGAA 5411
       ||||| ||||| ||||| |||||
Db      1 AAAAAAAAAAAAAAAAAA 19

RESULT 710
LOCUS   CL693186              19 bp DNA linear GSS 10-JUL-2004
DEFINITION PR10160C.B05.2 - PR10160C.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL693186
VERSION   CL693186.1 GI:50215094
KEYWORDS  GSS.
SOURCE    Pristionchus pacificus
ORGANISM  Pristionchus pacificus
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
AUTHORS   1 (bases 1 to 19)
TITLE     Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. Appends an Acceid database for the nematode satellite organism Pristionchus pacificus
JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT   Contact: Sommer RJ
           Evolutionary Biology
           Max-Planck-Institute for Developmental Biology
           Spemannstr. 37-39, Tuebingen D-72076, Germany
           Tel.: 00497071601371
           Fax: 00497071601498
           Email: ralf.sommer@uebingen.mpg.de
           This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
           Seq primer: T7
           Class: Fosmid ends.
FEATURES             Location/Qualifiers
     source            1..19
                        /organism="Pristionchus pacificus"
                        /mol_type="genomic DNA"
                        /strain="California"
                        /db_xref="taxon:54126"
                        /clone_lib="Mixed stage fosmid library of P. pacificus var. California"
                        /note="Vector: pGP1fos-5 Fosmid vector"
Query Match          0.3% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0

OY      5393 AAAAAAAAAACAAAGGAA 5411
       ||||| ||||| ||||| |||||
Db      1 AAAAAAAAAAAAAAAAAA 19

RESULT 711
LOCUS   CL693191              19 bp DNA linear GSS 10-JUL-2004
DEFINITION PR10160C.H08.2 - PR10160C.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION   CL693191.1 GI:50215099
KEYWORDS  GSS.
SOURCE    Pristionchus pacificus

```

```

ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS
Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
Appadri: an Acedb database for the nematode satellite organism
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RU
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foemid ends.

FEATURES
source
location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/collection="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pGpifos-5 Fosmid vector"

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 0.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAA 5411
||||| ||||| ||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 712
AL038460 20 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION
DKFZP566B2246.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
AL038460
AL038460
AL038460.1 GI:49682131
EST.
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Ostenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,U. and
Wiemann,S.
TITLE
EST (Ostenwaelder, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/collection="DKFZP566B2246"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2Biu"
/collection="566 (synonym: hfkcd2)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 0.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      5402 CAAAAAGAAAAATGAA 5420
Db      2 CAAAAAGAAAAA 20

RESULT 713
AL587572/c 20 bp mRNA linear EST 02-MAR-2001
LOCUS      AL587572/c
DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  ROS059B11, mRNA sequence.
VERSION     AL587572
KEYWORDS    AL587572.1 GI:13192606
SOURCE      EST.
ORGANISM    Gallus gallus (chicken)
            Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 20)

REFERENCE
AUTHORS     Murray, F.
TITLE       BP Chicken Brain Library
JOURNAL     Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bsrc.ac.uk
            GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
            (*6854-

Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes=vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

FEATURES
source
Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5402 CAAAAAGAAAAATGAA 5420
Db      19 CAAAAAGAAAAA 1

RESULT 714
AL587727/c 20 bp mRNA linear EST 02-MAR-2001
LOCUS      AL587727/c
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  ROS061D01, mRNA sequence.
VERSION     AL587727
KEYWORDS    AL587727.1 GI:13192761
SOURCE      EST.
ORGANISM    Gallus gallus (chicken)
            Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 20)

REFERENCE
AUTHORS     Murray, F.

```

```

TITLE      BP Chicken Brain Library
JOURNAL    Unpublished (2001)
COMMENT    Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bsrc.ac.uk
            GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
            (*6854-

FEATURES
source
Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5398 AATACAAAAAGAAAAAT 5416
Db      19 AAAAAAGAAAAA 1

RESULT 715
AL587759/c 20 bp mRNA linear EST 02-MAR-2001
LOCUS      AL587759/c
DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  ROS061G06, mRNA sequence.
VERSION     AL587759
KEYWORDS    AL587759.1 GI:13192793
SOURCE      EST.
ORGANISM    Gallus gallus (chicken)
            Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 20)

REFERENCE
AUTHORS     Murray, F.
TITLE       BP Chicken Brain Library
JOURNAL     Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bsrc.ac.uk
            GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
            (*6854-

Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061G06"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes=vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCCGCTTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

FEATURES
source

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-A20"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5402 CAAAAGAAAATGAAA 5420
Db      ||||| ||||| |||
        19 CAAAAGAAAATGAAA 5411

RESULT 719
CF318278/c      20 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION      HD-08-F13.b1 OSHDA1-overexpressing transgenic rice plasmid CDNA
                  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                  HD-08-F13, mRNA sequence.
ACCESSION
VERSION          CF318278
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-F13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
```

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Db      20 AAAAAAAAAAAAAAAAAA 2
        ||||| | ||||| ||

RESULT 720
CF319428/c      20 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION      HD-09-O20.b1 OSHDA1-overexpressing transgenic rice plasmid CDNA
                  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                  HD-09-O20, mRNA sequence.
ACCESSION
VERSION          CF319428
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-O20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source

Query Match      0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5391 TTAATAAATACAAAAAG 5409
Db      ||||| ||||| |||||
        19 TCAAAAAAAAAAAAAAAAAAG 1

RESULT 721
CF320843/c      20 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION      HD-11-001.g1 OSHDA1-overexpressing transgenic rice plasmid CDNA
                  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                  HD-11-001, mRNA sequence.
ACCESSION
VERSION          CF320843
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
```

TITLE Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
COMMENT Unpublished (2003)  
Contact: Nahm, B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-11-001"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

Query Match 0.3%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAGAAAGAAAATGAAA 5420  
|||||  
Db 20 CAAAAAAAAAAAAAAAAAAAA 2

# RESULT 722

AZ68518

LOCUS 20 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0118G09R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0118G09 R, genomic survey sequence.

ACCESSION AZ68518

VERSION A2626475.1 GI:10482218

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiser, R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0118 row: G column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

FEATURES

source

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/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"


/clone_lib="Mouse 10kb plasmid UUC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114[gb]AP129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."


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Query Match 0.3%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAA 5407  
|||||  
Db 2 ATTAAAAAACAACAAAA 20

# RESULT 723

AZ626475

LOCUS 20 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0466E16R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0466E16 R, genomic survey sequence.

ACCESSION AZ626475

VERSION A2626475.1 GI:11748665

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiser, R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0466 row: E column: 16

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

FEATURES

source

/db\_xref="taxon:10090"  
/clone="UGCIM0498E13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCIW library"  
/note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4606 CAGTGTGAGCCGAGAGC 4624  
Db 19 CCGCGCTGAGCCGAGAGC 1

RESULT 724  
AZ638704 AZ638704 20 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0498E13R Mouse 10kb plasmid UGCIW library Mus musculus genomic  
DEFINITION clone UGCIW0498E13 R, genomic survey sequence.  
ACCESSION AZ638704  
VERSION AZ638704.1 GI:11760894  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0498 row: B column: 13  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UGCIM0498E13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCIW library"  
/note="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAATACAAAAGAA 5411  
Db 2 AAAAAAAAAAAAAAAAAA 20

RESULT 725  
AZ821905 AZ821905 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0094D20R Mouse 10kb plasmid UGCIW library Mus musculus genomic  
DEFINITION clone UGCIW200094D20 R, genomic survey sequence.  
ACCESSION AZ821905  
VERSION AZ821905.1 GI:12991813  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0094 row: D column: 20  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UUGC2M0094D20"  
 /sex="Male"  
 /lab host="E. Coli strain X110-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5402 CAAAAAGCAAAATGAAA 5420  
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 2 CAAAAAGCAAAATGAAA 20

RESULT 726  
 AM248574 17 bp mRNA linear EST 07-JAN-2000  
 LOCUS AM248574/c  
 DEFINITION 2821096.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821096 3',  
 mRNA sequence.

ACCESSION AM248574 GI:6591567  
 VERSION AM248574.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 17)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other\_ESTs: 2821096.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNI at:  
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
 PHRED high quality bases following vector sequence. Very Low  
 Quality Sequence: Trace file contained 17 contiguous distinct peaks  
 following vector sequence. Polyadenylation: Based upon the presence  
 of a XhoI site followed by a run of 14 or more T residues at the  
 beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: L10M5 row: 0 column: 17  
 High quality sequence stop: 8.  
 Location/Qualifiers  
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/mol type="mRNA"  
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 /cell\_line="MGC3"  
 /lab host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
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 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5396 AAAATCAAAAAGAAA 5412  
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 17 AAAATCAAAAAGAAA 1

RESULT 727  
 BQ590128 17 bp mRNA linear EST 06-DEC-2002  
 LOCUS BQ590128/c  
 DEFINITION E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris  
 cDNA clone 024-019-E19-819-819-PRIME, mRNA sequence.

ACCESSION BQ590128 GI:26119711  
 VERSION BQ590128.1  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 17)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
 and Radolof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mplz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 19 row: B column: 19  
 Seq primer: T7; GTATACGACCTCACTATAGGCG.  
 Location/Qualifiers  
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 line)"  
 /db\_xref="GABI:189986"  
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 /lab host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinfanzleben Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:

FEATURES  
 source

FEATURES  
 source

SP6-Sall-CCAGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2;

QY 5392 TAAATAAATACAAAAA 5408  
17 TAAAAAAAAAAAAAAAAA 1

RESULT 728  
B0591181/c  
LOCUS  
DEFINITION B0591181 17 bp mRNA linear EST 06-DEC-2002  
E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION B0591181  
VERSION B0591181  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert length: 17 Std Error: 0.00  
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Location/Qualifiers

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Kleinanzeleber Saatnucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and  
orientation:  
Spe-Sall-CCAGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

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QY 5399 ATACAAAAAGAAAA 5415  
17 ATAAAAAAAAAAAAAAAA 1

RESULT 729  
CF276637  
LOCUS  
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14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) CDNA clone 14ETL--01-N18,  
mRNA sequence.

ACCESSION CF276637  
VERSION CF276637  
KEYWORDS CF276637.1 GI:33654023  
SOURCE EST.  
ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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Matches 15; Conservative 0; Mismatches 2;

QY 5397 AATACAAAAAGAAAA 5413  
17 AAAAAAAAAAAAAAAAAA 1

RESULT 730  
CF294668/c  
LOCUS  
DEFINITION CF294668 17 bp mRNA linear EST 14-AUG-2003  
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) CDNA clone 30DGS--04-E17, mRNA  
sequence.

ACCESSION CF294668  
VERSION CF294668.1 GI:33663701  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Enharitoidae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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QY 5392 TAAATAATACAAAAA 5408  
Db 17 TAAAAAAAAAAAAAAAAA 1

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DEFINITION CF295988 17 bp mRNA linear EST 14-AUG-2003  
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) CDNA clone 30DGS--06-C17, mRNA  
sequence.  
ACCESSION CF295988  
VERSION CF295988.1 GI:33665021  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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with oligoribonucleotides and then used as templates for  
RT-PCR."

REFERENCE  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5392 TAAATAATACAAAAA 5408  
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 732  
LOCUS CF319075/c 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--09-H06.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) CDNA clone  
HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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line."

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5399 ATACAAAAAGAAAAA 5415  
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 733  
LOCUS CF336950/c 17 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--07-D04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone  
JMT--07-D04, mRNA sequence.  
ACCESSION CF336950  
VERSION CF336950.1 GI:33822280  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

REFERENCE  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
TITLE         Contact: Nahm B.H.
COMMENT       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5392 TTAATAAATTCATAAAA 5408
Db      17 TTAATAAATAAAAAAAAAA 1

RESULT 734
CF302409/c 18 bp mRNA linear EST 15-AUG-2003
LOCUS       7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA
sequence.
ACCESSION   CF298591
VERSION     CF298591
KEYWORDS    CF298591.1 GI:33670352
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
AUTHORS     Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
TITLE         Contact: Nahm B.H.
COMMENT       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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QY      5392 TTAATAAATTCATAAAA 5408
Db      18 TTAATAAATAAAAAAAAAA 2

RESULT 735
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LOCUS       7LEAF--05-01 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-005, mRNA
sequence.
ACCESSION   CF301151
VERSION     CF301151.1 GI:33672912
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
AUTHORS     Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
TITLE         Contact: Nahm B.H.
COMMENT       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA
sequence.
ACCESSION      CF302409
VERSION        CF302409.1  GI:33674170
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, Greengene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Query Match      0.3%; Score 13.8; DB 1; Length 18;
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LOCUS        HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION   HD--10-M11, mRNA sequence.
ACCESSION    CF320046
VERSION      CF320046.1  GI:33691807
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, Greengene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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      18 ATAAAAAAGAAAAA 2

RESULT 738
CF320418      18 bp      mRNA      linear      EST 15-AUG-2003
LOCUS        HD--11-E22.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION   HD--11-E22, mRNA sequence.
ACCESSION    CF320418
VERSION      CF320418.1  GI:33692179
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, Greengene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
               Location/Qualifiers
               1..18
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="HD--11-E22"
               /tissue_type="callus"
               /dev_stage="proliferated callus on 2M6 media for 2 weeks"
               /lab_host="E.coli DH10B"
               /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
               cDNA library (HD)"
               /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
               treated with ABA(20um) for 1hr. Oligo-capped mRNA was
               reverse transcribed and then used for PCR. mRNA was
               derived from rice Histone Deacetylase overexpression
               line."

FEATURES
source

```

QY 5393 AAAAAAAAAAAG 5409  
 |||||  
 Db 17 AAAAAAAAAAAAAA 1

RESULT 739  
 CF278272/c  
 LOCUS CF278272 19 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01,  
 mRNA sequence.  
 CF278272  
 ACCESSION CF278272.1 GI:33655658  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 TITLE  
 JOURNAL  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source  
 1. 19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cuiivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="14ETL--04-C01"  
 /cissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_11b="Rice etiolated leaf plasmid cDNA library  
 (14ETL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5391 TTAATAAATGCAAAA 5407  
 |||||  
 Db 17 TTAATAAATGCAAAA 1

RESULT 740  
 AZ360314  
 LOCUS AZ360314 19 bp DNA linear GSS 02-OCT-2000  
 DEFINITION IM0103G03R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0103G03 R, genomic survey sequence.  
 ACCESSION AZ360314  
 VERSION AZ360314.1 GI:10474014  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE  
 JOURNAL  
 COMMENT Niederhausern,A. and Wright D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0103 row: G column: 03  
 Seq primer: CACACAGAAACACCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

FEATURES  
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 1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCG1M0103G03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_11b="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (G1473214|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E.coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 4.5e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5409 GAAATAATGAAATTA 5425  
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 Db 1 GAAATAATGAAATAA 17

RESULT 741  
 AZ432757  
 LOCUS AZ432757 19 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0218L14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0218L14 F, genomic survey sequence.  
 ACCESSION AZ432757  
 VERSION AZ432757.1 GI:10556770  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
**JOURNAL** Plasmid inserts  
**COMMENT** Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0218 row: L column: 14  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0218L14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**FEATURES**  
**source**  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match** 0.3%; Score 13.8; DB 1; Length 19;  
**Best Local Similarity** 88.2%; Pred. No. 4.5e+02;  
**Matches** 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 2568 CGAGAGAGAGATCGAGA 2584  
|||||  
1 CGAGAGCGAGAGCGAGA 17

**Db** 1 CGAGAGCGAGAGCGAGA 17

**RESULT 742**  
**AZ447251/c** 19 bp DNA linear GSS 04-OCT-2000  
**LOCUS** 1M0244J19P Mouse 10kb plasmid UUC1M library Mus musculus genomic  
**DEFINITION** clone UUC1M0244J19 F, genomic survey sequence.  
**ACCESSION** AZ447251  
**VERSION** AZ447251.1 GI:10599050  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 19)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL** Plasmid inserts  
**COMMENT** Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: J column: 19  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0244J19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**FEATURES**  
**source**  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**Query Match** 0.3%; Score 13.8; DB 1; Length 19;  
**Best Local Similarity** 88.2%; Pred. No. 4.5e+02;  
**Matches** 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 5399 ATACAAAAGAGAAAAA 5415  
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17 ATAAAAAAGAGAAAAA 1

**Db** 17 ATAAAAAAGAGAAAAA 1

**RESULT 743**  
**AZ450180** 19 bp DNA linear GSS 04-OCT-2000  
**LOCUS** 1M0248K13R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
**DEFINITION** clone UUC1M0248K13 R, genomic survey sequence.  
**ACCESSION** AZ450180  
**VERSION** AZ450180.1 GI:10604710  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 19)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts





Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gdbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

# FEATURES

source

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1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="14ROOT-01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.2%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAA 5407  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAA 15

RESULT 748  
 BQ593528/c 17 bp mRNA linear EST 06-DEC-2002  
 LOCUS S015525-024-026-123-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 DEFINITION cDNA clone 024-026-123 5-PRIME, mRNA sequence.  
 ACCESSION BQ593528  
 VERSION BQ593528.1 GI:26123111  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

# REFERENCE

Authors: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 17)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Dzungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Kadelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 JOURNAL fingerprinting allows access to 25 000 potential sugar beet genes  
 MEDLINE Plant J. 32 (5), 845-857 (2002)  
 PUBMED 22362189  
 COMMENT 12472698  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 26 Row: 1 Column: 23  
 Seq primer: SP6; CATACGATTAGCTGACACTATAG.  
 Location/Qualifiers

# FEATURES

source

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/mol_type="mRNA"
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line)"
/db_xref="GABI:193326"
/db_xref="taxon:161934"
/clone="024-026-123"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzelebener Saatzzucht AG Einbeck, Germany, contact:

```

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1181 GAGGAAGAGAGAG 1195  
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 Db 15 GAGGAGAGAGAGAG 1

RESULT 749  
 BM658677/c 18 bp mRNA linear EST 27-FEB-2002  
 LOCUS LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION BM658677  
 VERSION BM658677.1 GI:18958948  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 18)  
 Adelson,D.L. and Gill,C.A.  
 Porcine ESTs  
 Unpublished (2002)  
 Contact: David L. Adelson  
 Animal Breeding and Genetics  
 Texas A&M University  
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
 USA  
 Tel: 9798452616  
 Fax: 9798456970  
 Email: david.adelson@tamu.edu.

# FEATURES

source

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1. .18
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSEQFXL37 pig adrenal"
/note="Organ: adrenal gland; Vector: pBluescript SK+;
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCCAATTGAGCTCACCGGCGGCGCGCGCTCGAG. Sequence 3' of
the inserts (AAGAAATTCGATTCACCTTATCGATCCGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."

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Query Match 0.2%; Score 13.4; DB 1; Length 18;  
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5401 ACAGAGAGAGAG 5415  
 |||||  
 Db 17 AAAAAAAAAAGAAAAA 3

RESULT 750  
 AZ447864/c 19 bp DNA linear GSS 04-OCT-2000  
 LOCUS IM0245A14F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 DEFINITION clone UUC1M0245A14 F, genomic survey sequence.  
 ACCESSION AZ447864  
 VERSION AZ447864.1 GI:10600087  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

# ORGANISM

Mus musculus

REFERENCE	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Dunn,D., Loygaci,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reller,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0245 row: A column: 14 Seq primer: CGTGTAAACGACGGCAGT Class: plasmid ends High quality sequence stop: 19. location/Qualifiers
FEATURES	1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCIM0245A14" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb Purified UUCIM library" /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
SOURCE	Query Match                 0.2%; Score 13.4; DB 1; Length 19; Best Local Similarity     93.3%; Pred. No. Se+O2; Matches     14; Conservative     0; Mismatches     1; Indels     0; Gaps     0;
Oy	5411 AAAATGAATAATAA 5425
Db	17 AAAATGAATAATAA 3
RESULT 751	
LOCUS	AL038692
DEFINITION	AL038692 18 bp mRNA linear EST 06-JUL-2004
ACCESSION	DKFZps66J0846.r1.566 (synonym: htfcd2) Homo sapiens cDNA clone
VERSION	DKFZps66J0846.mRNA sequence.
KEYWORDS	AL038692 AL038692.1 GI:49682190
ORGANISM	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

	REFERENCE	Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
AUTHORS	Ostenwalder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.	
TITLE	EST (Ostenwalder, et al.)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: MIPS	
FEATURES	Ingoletae dter Landstr. l, D-85764 Neuherberg, Germany. Location/Qualifiers . . 18 /organism= "Homo sapiens" /mol_type= "mRNA" /db_xref= "taxon:9606" /cclone= "DKFZps566J0846" /class_type= "Kidney" /dev_stage= "fetal" /lab_host= "Xl-2biue" /clone_lib= "566 (synonym: hfkd2)" /note= "Vector: pAMP1; Site_1: NotI; Site_2: SalI"	
Query Match	0.2%; Score 13.2; DB 1; Length 18;	
Best Local Similarity	83.3%; Pred. No. 5e+02;	
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	5398 AATGCAAAAGAAAAA 5415              Db 1AAAAAAAAAAAAAAAAAAA 18	
RESULT 752		
LOCUS	AL048754                18 bp       mRNA         linear EST 04-SEP-2003	
DEFINITION	DKFZPS66L173.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone	
ACCESSION	DKFZPS66L173.mRNA sequence.	
VERSION	AL048754	
KEYWORDS	AL048754.1 GI:4727825	
SOURCE	EST.	
ORGANISM	Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	1 (bases 1 to 18) Koehler, K., Meyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehler, et al.) Unpublished (1999) Contact: MIPS	
COMMENT	Ingoletae dter Landstr. l, D-85764 Neuherberg, Germany. Location/Qualifiers . . 18 /organism= "Homo sapiens" /mol_type= "mRNA" /db_xref= "taxon:9606" /cclone= "DKFZPS66L173" /class_type= "kidney" /dev_stage= "fetal" /lab_host= "Xl-2biue" /clone_lib= "566 (synonym: hfkcd2)" /note= "Vector: pAMP1; Site_1: NotI; Site_2: SalI"	
Query Match	0.2%; Score 13.2; DB 1; Length 18;	
Best Local Similarity	83.3%; Pred. No. 5e+02;	
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	5391 TTAATAAAATTCAA AAAA 5408              Db 1TCAAAAAAAAAAAAAAAAAAA 18	
RESULT 753		
LOCUS	AM246505                18 bp       mRNA         linear EST 07-JAN-2000	
Accession	AM246505/C	

DEFINITION 2821585.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821585 3', mRNA sequence.

ACCESSION AM246505

VERSION AM246505.1 GI:6589498

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Other ESTs: 2821585.5prime

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@wmail.nih.gov](mailto:cgapsb@wmail.nih.gov)

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing project

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www.bio.lnl.gov/bdip/image/image.html](http://www.bio.lnl.gov/bdip/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CMT7 row: D column: 2

High quality sequence stop: 18.

Location/Qualifiers

1. 18

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2821585"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_id="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5397 AATACCAAAAGAAAAA 5414

Db 18 AATATTAAGAAAAA 1

RESULT 754

BO582676 18 bp mRNA linear EST 06-DEC-2002

LOCUS BO582676

DEFINITION E012281-024-007-P18-SPE MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION BO582676

VERSION BO582676.1 GI:26112253

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 18)

Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Leirach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

CONTACT: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weishaar@mpiz-koeln.mpg.de](mailto:weishaar@mpiz-koeln.mpg.de)

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATCAGATTAGCTACACTATAG.

Location/Qualifiers

1. 18

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:184018"

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/clone="024-007-P18"

/tissue\_type="inflorescence"

/lab\_host="EMDH10B"

/clone\_id="MP1Z-ADIS-024-inflorescence"

/note="Vector: PCWVS/POR6; Site\_1: SalI; Site\_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnlebeher Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5398 AATCAAAAGAAAAA 5415

Db 18 AAAAAAAGAAAAA 1

RESULT 755

BO590027 18 bp mRNA linear EST 06-DEC-2002

LOCUS BO590027

DEFINITION E012844-024-019-E24-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BO590027

VERSION BO590027.1 GI:26119610

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 18)

Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Leirach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)



**MEDLINE** 22362189  
**PUBMED** 12472698  
**COMMENT** Contact: Weisshar B  
1973-1974

FEATURES	Location/Qualifiers
source	1. .18

Query Match	0.2%	Score 13.2	DB 1	length 18
Best Local Similarity	83.3%	Pred No. 5e+02		
Matches 15, Conservative	0	Mismatches 3	Indels 0	Gaps 0

FEATURES	Location/Qualifiers
Source	1. 18
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--03-J04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="rice etiolated leaf plasmid cDNA library
14ETL1"
/note="vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.2%	Score 13.2;	DB 1;	Length 18;
Best Local Similarity	83.3%	Pred. NO. 5e+02;		
Matches	15;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	5398	AATCAAAAGGAAAAA	5415	
Db	18	AAAAAAAAAAAAAAAAA	1	

TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr
FEATURES	Location/Qualifiers
SOURCE	1. 18

Query Match	0.2%	Score 13.2	DB 1	Length 16
Best Local Similarity	83.3%	Pred. No. 5e+02		
Matches 15, Conservative	0	Mismatches 3	Indels 0	Gaps 0

RESULT 758  
CF299027/C

LOCUS CF299027 18 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-N14, mRNA sequence.  
 ACCESSION CF299027  
 VERSION CF299027.1 GI:33670788  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
 source  
 1..18  
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 /db\_xref="taxon:39947"  
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 /lab\_host="E.coli DH10B"  
 /clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
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Query Match 0.2%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATCAAAAAAGAAAAA 5415  
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 759  
 LOCUS CF299674/c 18 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA sequence.  
 ACCESSION CF299674  
 VERSION CF299674.1 GI:33671435  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355

FEATURES  
 source  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--03-M14"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATCAAAAAAGAAAAA 5415  
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 760  
 LOCUS CF300456/c 18 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA sequence.  
 ACCESSION CF300456  
 VERSION CF300456.1 GI:33672217  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 18)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..18  
 /organism="Oryza sativa (japonica cultivar-group)"  
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 /cultivar="Nackdong"  
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 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_1lb="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5408 AGAAAAATGAAATATA 5425  
 Db 18 AGAAAAAAAAAAAAAAAA 1

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RESULT 761
CF301325/c
LOCUS
DEFINITION
CF301325 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-C12, mRNA
sequence.
ACCESSION
CF301325
VERSION
CF301325.1 GI:33673086
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..18
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.2%; Score 13.2; DB 1; Length 18;
Beet Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5398 AATACAAAAGAAAAA 5415
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 762
CF301760/c
LOCUS
DEFINITION
CF301760 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
sequence.
ACCESSION
CF301760
VERSION
CF301760.1 GI:33673521
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division

```

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-L22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source
Query Match 0.2%; Score 13.2; DB 1; Length 18;
Beet Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5398 AATACAAAAGAAAAA 5415
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 763
CF309376/c
LOCUS
DEFINITION
CF309376 18 bp mRNA linear EST 15-AUG-2003
ABF--03-119.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-119, mRNA sequence.
ACCESSION
CF309376
VERSION
CF309376.1 GI:33681137
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--03-119"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.2%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 18 AGTAAAAA 1

Db 18 AGTAAAAA 1

RESULT 764  
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 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA  
 sequence.  
 ACCESSION CF329484 GI:33807207  
 VERSION CF329484.1  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
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 /rissue\_type="callus"  
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 /lab\_host="E.coli DH10B"  
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 RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;  
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 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 18 AGTAAAAA 1

RESULT 765  
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 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA  
 sequence.  
 ACCESSION CF329485 GI:33807209  
 VERSION CF329485.1  
 KEYWORDS Oryza sativa (japonica cultivar-group)  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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Query Match 0.2%; Score 13.2; DB 1; Length 18;  
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Db 1 AGTAAAAA 18

RESULT 766  
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 LOCUS IM0218L14F Mouse 10kb plasmid tUGCIM library Mus musculus genomic  
 DEFINITION clone UUDC1M0218L14 F, genomic survey sequence.  
 ACCESSION AZ432757  
 VERSION AZ432757.1 GI:10556770  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0218 row: L column: 14  
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 Class: plasmid ends  
 High quality sequence stop: 19.  
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/clone="U06C1M0218L14"  
/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and high molar excess of 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 229 CCTCACCCTCACCCTCC 246  
DB 19 CCTCTCCTCTCCTCTC 2

RESULT 767  
A1590540  
LOCUS 16 bp mRNA linear EST 14-MAY-1999  
DEFINITION tw11c02.x1 NCI CGAP Brn52 Homo sapiens CDNA clone IMAGE:225362 3'  
VERSION A1590540  
ACCESSION A1590540.1 GI:4599588  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BrTAP), Tumor Gene Index  
Unpublished (1998)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga9b@remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLML at: www-bio.lnlnl.gov/bbrp/image/image.html

FEATURES  
source 1..16  
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/note="Organ: brain; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; This library represents the normalized version of NCI CGAP Brn52. Cloned unidirectionally.  
Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV).  
Constructed by Life Technologies."

Query Match 0.2%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1270 CCCGACCCACACAC 1282  
DB 3 CCCGACCCACACAC 15

RESULT 768  
A1569544  
LOCUS 16 bp mRNA linear EST 12-MAY-1999  
DEFINITION to28d10.x1 NCI CGAP ut4 Homo sapiens CDNA clone IMAGE:2180371 3'  
VERSION A1569544  
ACCESSION A1569544.1 GI:4532918  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga9b@remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLML at: www-bio.lnlnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1683 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 1  
POLYA=No.

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Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 227 CCCCTCACTCACC 242  
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 Db 1 CCCCTCCCCCACC 16

RESULT 769  
 B0590166/c 16 bp mRNA linear EST 06-DEC-2002  
 LOCUS DEFINITION B012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 B0590166 CNA clone 024-019-K18 3-PRIME, mRNA sequence.  
 ACCESSION B0590166  
 VERSION B0590166.1 GI:26119749  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radehof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 19 row: K column: 18  
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 Location/Qualifiers  
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 /lab\_host="EMDH10B"  
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 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 5e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAA 5408  
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 Db 16 AAAAAAAAAAAAAA 1

RESULT 770  
 B0590507/c 16 bp mRNA linear EST 06-DEC-2002  
 LOCUS DEFINITION B0590507

DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 CNA clone 024-019-M04 3-PRIME, mRNA sequence.  
 ACCESSION B0590507  
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 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radehof,U.  
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 Plant J. 32 (5), 845-857 (2002)

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 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /db\_xref="GABI:189608"  
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 /lab\_host="EMDH10B"  
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 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebeener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 5e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 771  
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 LOCUS DEFINITION S013686-024-028-F08-SP6R MP1Z-ADIS-024-developing root Beta vulgaris  
 B0592600 CNA clone 024-028-F08 5-PRIME, mRNA sequence.  
 ACCESSION B0592600  
 VERSION B0592600.1 GI:26122183  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT  
 Contact: Weisshaar B  
 ADIS DNA core facility at MPiZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
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 /note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinfanzlebener Saatnucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 5e+02;  
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RESULT 772  
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 LOCUS S013324-024-028-A01-T7 MPiZ-ADIS-024-developing root Beta vulgaris  
 DEFINITION cDNA clone 024-028-A01 3-PRIME, mRNA sequence.  
 ACCESSION B0592965  
 VERSION B0592965.1 GI:26122548  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT  
 Contact: Weisshaar B

ADIS DNA core facility at MPiZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 28 row: A column: 01  
 Seq primer: T7; GTAATAGACTCACTATAGGAC.  
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 cDNA library from sugar beet, library provided by KWS  
 Kleinfanzlebener Saatnucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
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 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 16 AAAAAAAAAAAAAA 1

RESULT 773  
 B0595369/c 16 bp mRNA linear EST 06-DEC-2002  
 LOCUS S013317-024-022-P02-T7 MPiZ-ADIS-024-developing root Beta vulgaris  
 DEFINITION cDNA clone 024-022-P02 3-PRIME, mRNA sequence.  
 ACCESSION B0595369  
 VERSION B0595369.1 GI:26124952  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT  
 Contact: Weisshaar B  
 ADIS DNA core facility at MPiZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
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/note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleimanzelebener Saatzzucht AG Eibbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
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# RESULT 774

LOCUS B0595717 16 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
CNDA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION B0595717  
VERSION B0595717.1 GI:26125300  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drunowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

## COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;  
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QY 5393 AAAAAATACAAAAA 5408  
1 AAAAAAAAAAAAAA 16

RESULT 775  
LOCUS CF279325/c 16 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09, mRNA sequence.

ACCESSION CF279325  
VERSION CF279325.1 GI:33656711  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAA 5408  
16 AAAAAAAAAAAAAA 1

RESULT 776  
CF296130/c



LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 300GS--06-F22.b1 Rice leaf plasmid cDNA library I (300GS) Oryza sativa (japonica cultivar-group) cDNA clone 300GS--06-F22, mRNA sequence.  
 ACCESSION CF296130 GI:33665163  
 VERSION CF296130.1  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
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Query Match 0.2%; Score 12.8; DB 1; Length 16;  
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 DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-C03, mRNA sequence.  
 ACCESSION CF311057  
 VERSION CF311057.1 GI:33682818  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

FEATURES  
 source  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 Db 16 AAAAAAATACAAAAA 1

RESULT 778  
 LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--02-G01.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--02-G01, mRNA sequence.  
 ACCESSION CF314013  
 VERSION CF314013.1 GI:33685774  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
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Best Local Similarity 87.5%; Pred. No. 5e+02; DB 1; length 16;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 16 TAAAAAAGCAAAAAA 1

RESULT 779  
CF314377/c 16 bp mRNA linear EST 15-AUG-2003

LOCUS  
DEFINITION HD--02-001.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--02-001, mRNA sequence.

ACCESSION  
VERSION CF314377.1 GI:33686138  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
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line."

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Db 16 AAAAAAAGCAAAAAA 1

RESULT 780  
CF315789/c 16 bp mRNA linear EST 15-AUG-2003

LOCUS  
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HD--04-N10, mRNA sequence.

ACCESSION  
VERSION CF315789.1 GI:33687550  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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line."

Query Match 0.2%; Score 12.8; DB 1; length 16;  
Best Local Similarity 87.5%; Pred. No. 5e+02; DB 1; length 16;  
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Qy 5393 AAAAAAATACAAAAA 5408

Db 16 AAAAAAAGCAAAAAA 1

RESULT 781  
CF316056/c 16 bp mRNA linear EST 15-AUG-2003

LOCUS  
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HD--05-D07, mRNA sequence.

ACCESSION  
VERSION CF316056  
KEYWORDS  
SOURCE  
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Oryza sativa (japonica cultivar-group)  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
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line."

Query Match      0.2%: Score 12.8; DB 1; Length 16;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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16 AAAAAAAAAAAAAAAAAA 1

RESULT 782
CF317718      16 bp mRNA linear EST 15-AUG-2003
LOCUS
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-I05, mRNA sequence.
ACCESSION
CF317718
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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line."

Query Match      0.2%: Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAAAAA 1

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RESULT 783
CF320356      16 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--11-D14, mRNA sequence.
ACCESSION
CF320356
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--11-D14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.2%: Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAATACAAAAA 5408
| | | | | | | | | |
| | | | | | | | | |
16 AAAAAAAAAAAAAAAAAA 1

RESULT 784
CF327722      16 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
sequence.
ACCESSION
CF327722
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## SOURCE

Location/Qualifiers

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1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-F06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

OY 5393 AAAAAAATACAAAAA 5408

Db 16 AAAAAAAAAAAAAAAAAA 1

## RESULT 785

## LOCUS

CF329320/c 16 bp mRNA linear EST 18-AUG-2003

## DEFINITION

NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA  
sequence.

ACCESSION CF329320.1 GI:33806877

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## SOURCE

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1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.2%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

OY 5400 TACAAAAAGAAAAA 5415

Db 16 TAAAAAAAAAAAAAAAAA 1

## RESULT 786

## LOCUS

CF333386 16 bp mRNA linear EST 18-AUG-2003

## DEFINITION

JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--02-E05, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## SOURCE

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1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="JMT--02-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis thaliana Carboxyl
methyltransferase overexpression line."
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Query Match 0.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

OY 5393 AAAAAAATACAAAAA 5408

Db 1 AAAAAAAAAAAAAAAAAA 16

## RESULT 787

## LOCUS

AM247165/c 17 bp mRNA linear EST 07-JAN-2000

## DEFINITION

2819675.jprime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819675 3',  
mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

AM247165.1 GI:6590158  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 17)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other\_ESTRs: 2819675, 5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue procurement: DCTD/DRP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LNL at:  
[www.bic.lnl.gov/bbrp/image/image.html](http://www.bic.lnl.gov/bbrp/image/image.html) Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T identification: patch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 17  
 contiguous PHRED high quality bases following vector sequence. Very  
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 peaks following vector sequence.  
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 High quality sequence stop: 17.  
 Location/Qualifiers

#### FEATURES

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 /organism="Homo sapiens"  
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 /clone="IMAGE:2819675"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH-MGC 7"  
 /note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAACAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2% Score 12.8; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5397 AATATCAAAAGAAA 5412

DB 17 AAAAAAAAAAAAAA 2

**RESULT 788**  
**BO590687** 17 bp mRNA linear EST 06-DEC-2002  
**LOCUS** S013717-024-018-B24-T7 MP12-ADIS-024-storage root Beta vulgaris  
**DEFINITION** cDNA clone 024-018-B24 3-PRIME, mRNA sequence.  
**ACCESSION** BO590687  
**VERSION** BO590687.1 GI:26120270  
**KEYWORDS** EST.  
**SOURCE** Beta vulgaris  
**ORGANISM** Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
**REFERENCE** 1 (bases 1 to 17)  
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.  
 and Radelof, U.  
**TITLE** Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
**JOURNAL** Plant J. 32 (5), 845-857 (2002)  
**MEDLINE** 22362189  
**PUBMED** 12472698  
**COMMENT** Contact: Weishaar B

**ADIS DNA core facility at MP12**  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: [weishaar@mp12-koeln.mpg.de](mailto:weishaar@mp12-koeln.mpg.de)  
 Insert Length: 17 Std Error: 0.00  
 Plate: 18 row: B column: 24  
 Seg primer: T7; GTAATACGACTCACTATAGGCG.  
 Location/Qualifiers

#### FEATURES

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 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:161934"  
 /clone="024-018-B24"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 Project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2% Score 12.8; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAAAA 5408

DB 1 AAAAAAAAAAAAAA 16

**RESULT 789**  
**BO591177** 17 bp mRNA linear EST 06-DEC-2002  
**LOCUS** BO591177/c  
**DEFINITION** E013717-024-017-B22-T7 MP12-ADIS-024-storage root Beta vulgaris  
**ACCESSION** BO591177  
**VERSION** BO591177.1 GI:26120760  
**KEYWORDS** EST.  
**SOURCE** Beta vulgaris  
**ORGANISM** Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
**REFERENCE** 1 (bases 1 to 17)  
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.  
 and Radelof, U.  
**TITLE** Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
**JOURNAL** Plant J. 32 (5), 845-857 (2002)  
**MEDLINE** 22362189  
**PUBMED** 12472698  
**COMMENT** Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: [weishaar@mp12-koeln.mpg.de](mailto:weishaar@mp12-koeln.mpg.de)  
 Insert Length: 17 Std Error: 0.00  
 Plate: 17 row: B column: 22  
 Seg primer: T7; GTAATACGACTCACTATAGGCG.  
 Location/Qualifiers

#### FEATURES

1..17

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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188948"
/db_xref="taxon:161934"
/clone="024-017-B2"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPB/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.2%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAA 5408

Db 17 AAAAAAAAAAAAAA 2

RESULT 790  
BO591588/c

LOCUS BO591588 17 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012616-024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
VERSION BO591588  
KEYWORDS BO591588.1 GI:26121171  
SOURCE EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)

REFERENCE  
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,W., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

FEATURES

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

JOURNAL  
MEDLINE  
PubMed

COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: C column: 15  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
SOURCE

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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
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/db_xref="GABI:188532"
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/clone_lib="MP1Z-ADIS-024-storage root"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPB/GABI-Primary database: http://gabi.rzpd.de"
```

Query Match 0.2%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5403 AAAAAAGAAAAATGA 5418

Db 16 AAAAAAAAAAAAAA 1

RESULT 791  
CF290854/c

LOCUS CF290854 17 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-A21.B1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice Ests  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggi.com, bnhnm@bio.myongji.ac.kr.

COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggi.com, bnhnm@bio.myongji.ac.kr.

FEATURES

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

JOURNAL  
MEDLINE  
PubMed

COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
SOURCE

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location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-A21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
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Query Match 0.2%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAA 5408

Db 17 AAAAAAAAAAAAAA 2

RESULT 792  
CF295807/c

LOCUS CF295807 17 bp mRNA linear EST 14-AUG-2003

```

DEFINITION 30DGS--05-012.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-012, mRNA
            sequence.
ACCESSION  CF295807
VERSION    CF295807.1 GI:33664840
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
            1 (bases 1 to 17)
REFERENCE  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      Journal
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
            source
            1..17
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            /mol_type="mRNA"
            /cultiyar="Nackdong"
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            /clone="30DGS--05-012"
            /tissue_type="leaf"
            /dev_stage="30 days after germination"
            /lab_host="E.coli DH10B"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

RESULT 793
CF298589 17 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA
            sequence.
ACCESSION  CF298589
VERSION    CF298589.1 GI:33670350
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
            1 (bases 1 to 17)
REFERENCE  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      Journal
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

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Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

RESULT 794
CF299639 17 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA
            sequence.
ACCESSION  CF299639
VERSION    CF299639.1 GI:33671400
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
            1 (bases 1 to 17)
REFERENCE  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      Journal
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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            /lab_host="E.coli DH10B"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 17;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

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RESULT 795
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LOCUS 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
sequence.
ACCESSION CF302447 GI:33674208
VERSION CF302447.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 796
CF310219/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-M02, mRNA sequence.
ACCESSION CF310219 GI:33681980
VERSION CF310219.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

FEATURES
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5408
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 797
CF311499/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
ACCESSION CF311499 GI:33683260
VERSION CF311499.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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line."
Query Match          0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      5400 TACAAAAAGAAAAA 5415
Db      16 TAAAAAAGAAAAA 1

RESULT 798
CF313013/c
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-P19, mRNA sequence.
ACCESSION
CF313013
VERSION
KEYWORDS
CF313013.1 GI:33684774
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Euryalota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      5393 AAAAAATACAAAAA 5408
Db      16 AAAAAAAGAAAAA 1

RESULT 799
CF334566/c
LOCUS
DEFINITION
JMT--03-O13.g1 ACJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-O13, mRNA sequence.
ACCESSION
CF334566
VERSION
KEYWORDS
CF334566.1 GI:33817460
EST.

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SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
REFERENCE Bukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.  
AUTHORS 1. (bases 1 to 17)  
TITLE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
COMMENT Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 5.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5408  
DB 17 AAAAAAAAAAAAAAAAAA 2  

RESULT 800 CF301057 18 bp mRNA linear EST 15-AUG-2003  
LOCUS CF301057/c  
DEFINITION 7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA sequence.  
ACCESSION CF301057  
VERSION CF301057.1 GI:33672818  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
REFERENCE Bukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.  
AUTHORS 1. (bases 1 to 18)  
TITLE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
COMMENT Unpublished (2003)  
CONTACT: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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Query Match 0.2%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 5.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5408  
DB 17 AAAAAAAAAAAAAAAAAA 2

RESULT 801  
CF329285/c  
LOCUS  
DEFINITION  
CF329285 18 bp mRNA linear EST 18-AUG-2003  
NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF329285  
CF329285.1 GI:33806806  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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Query Match 0.2%; Score 12.8; DB 1; Length 18;  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5400 TACAAAAAGAAAAA 5415  
DB 18 TAGAAAAAAGAAAAA 3

RESULT 802  
AZ776487/c  
LOCUS  
AZ776487 27 bp DNA linear GSS 16-FEB-2001

DEFINITION  
2M0010G08F Mouse 10kb plasmid UNGCM library Mus musculus genomic  
clone UNGC2M0010G08 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
A2776487  
A2776487.1 GI:12904111  
GSS.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Nederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: G column: 08  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers

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/note="Vector: PWD42nv; Purified genomic DNA from M.  
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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gil473214[gil4732972.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 12.8; DB 1; Length 27;  
Best Local Similarity 70.8%; Pred. No. 7.2e+02;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 224 TCTCCCTCACCTTCACCTTCCT 247  
DB 26 TCTACTCTCTCTCTCTCTCTCT 3

RESULT 803  
AJ662980  
LOCUS  
DEFINITION  
AJ662980 21 bp mRNA linear EST 28-JUN-2004  
CSROBAN09 Sus scrofa cDNA clone C0000024\_P01, mRNA

sequence.  
ACCESSION AJ662980  
VERSION AJ662980.1 GI:49347103  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pbuescriptII(KS+). R. Site 1: Ecort R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
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/clone\_lib="CSEORAN09"  
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Best Local Similarity 78.9%; Pred. No. 6.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 569 TGAAGAAGAGAGAGCTGAA 587  
Db 3 TGAAGAAGTGGGATGCA 21  
RESULT 804  
AZ342914 26 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0076C22F Mouse 10kb plasmid UUCGIM library Mus musculus genomic  
DEFINITION clone UUCGIM0076C22 F, genomic survey sequence.  
ACCESSION AZ342914  
VERSION AZ342914.1 GI:10420628  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: C column: 22  
Seq primer: CGTGTAAAGACGACGACG  
Class: plasmid ends  
High quality sequence stop: 26.  
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/db\_xref="taxon:10090"  
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/sex="Male"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD4 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.2%; Score 12.6; DB 1; Length 26;  
Best Local Similarity 78.9%; Pred. No. 7.4e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 969 AGAATCTTCCTCCTCCTC 987  
Db 1 AGAATCTTCCTCCTCCTC 19  
RESULT 805  
AZ873739 27 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0187C08R Mouse 10kb plasmid UUCGIM library Mus musculus genomic  
DEFINITION clone UUCG2M0187C08 R, genomic survey sequence.  
ACCESSION AZ873739  
VERSION AZ873739.1 GI:13082111  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



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DEFINITION      14ROOT-01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
                  sativa (japonica cultivar-group) cDNA clone 14ROOT-01-A17, mRNA
                  sequence.
ACCESSION       CF290849
VERSION         CF290849.1 GI:33659882
KEYWORDS        EST.
SOURCE          Oryza sativa (japonica cultivar-group)
ORGANISM        Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Eubartoideae; Oryzaceae; Oryza.
                1 (bases 1 to 15)
REFERENCE       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,T.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
TITLE          JOURNAL
COMMENT        Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..15
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                RT-PCR."

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Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5395 AAAAATACAAAAA 5408
        |||||
        1 AAAAAATAAAAAA 14

RESULT 809
LOCUS      CF296652                15 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
                  sativa (japonica cultivar-group) cDNA clone 30DGS--07-C02, mRNA
                  sequence.
ACCESSION   CF296652
VERSION     CF296652.1 GI:33665685
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eubartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 15)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      JOURNAL
COMMENT    Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
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  /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
  /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

Query Match      0.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5402 CAAAAAGAAAAA 5415
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RESULT 810
LOCUS      AU695224/C                16 bp      mRNA      linear      EST 29-JUN-2004
DEFINITION AU695224 KN261 Bos taurus cDNA clone KN261-046_F05, mRNA sequence.
ACCESSION   AU695224
VERSION     AU695224.1 GI:49428643
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 16)
REFERENCE   Anderson,S.I., Philpenson,H.A. and Archibald,A.L.
            Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
            Unpublished (2004)
TITLE      JOURNAL
COMMENT    Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross match with the -mnscore 20
            and -mismatch 12 options. Vector:pbLuescriptII(SK+) R. Site1: EcoRI
            R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
            bovine ovary. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
            EH25 9PS, www.atkgenomics.org.
            Location/Qualifiers
            1..16
            /organism="Bos taurus"
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            /clone="KN261-046_F05"
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            /clone_1lb="KN261"
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            SmaI; Single pass sequencing. Normalised library
            constructed from bovine ovary."

Query Match      0.2%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      38 CCAGCAGCCCGCGG 51
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        14 CCGCAGCCCGCGG 1

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RESULT 811  
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LOCUS E012843-024-019-015-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
DEFINITION CDNA clone 024-019-015 3-PRIME, mRNA sequence.  
ACCESSION BOS90207  
VERSION BOS90207.1 GI:26119790  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
AUTHORS 1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert length: 16 Std Error: 0.00  
Plate: 19 row: 0 column: 15  
Seq primer: T7: GTATACGACTCCTACTATAGAGC.  
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SP6-Sali-CCACGCGTCCG-5p-primr-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"  
Query Match 0.24; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 5.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORGANISM Oryza sativa (japonica cultivar-group)  
Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
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/lab\_host="E.coli DH10B"  
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Query Match 0.24; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 5.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 813  
CF327923/c 16 bp mRNA linear EST 18-AUG-2003  
LOCUS NCCL--02-J18.g1 Rice callus plasmid cDNA library (NCCL) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone NCCL--02-J18, mRNA sequence.  
ACCESSION CF327923  
VERSION CF327923.1 GI:33804096  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
REFERENCE Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
AUTHORS 1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
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/mol\_type="mRNA"

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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5402 CAAAAGAGAAAAA 5415
Db 16 CAAAAAAGAAAAA 3

RESULT 814
CF328223/c
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DEFINITION
  CF328223 16 bp mRNA linear EST 18-AUG-2003
  NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa (japonica cultivar-group) cDNA clone NACL--03-A10, mRNA
  sequence.
ACCESSION
  CF328223 GI:33804692
VERSION
  CF328223.1
KEYWORDS
  EST.
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 16)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, Greengene Biotech Inc., Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Gyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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    RT-PCR."

FEATURES
  source

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DEFINITION
  2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3',
  mRNA sequence.
ACCESSION
  AM250784
VERSION
  AM250784.1 GI:6593777
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2822335.5prime
  Contact: Robert Strauberg, Ph.D.
  Email: gga@nci.nih.gov
  Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (ILNI) DNA Sequencing by: Berkeley MGC sequencing
  project clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/ILNI at:
  www.bio.llnl.gov/dbp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
  Drosophila genome project. University of Washington Genome Center:
  http://www.genome.washington.edu/low/QualitySequence: 0 contiguous
  PHRED high quality bases following vector sequence. Very low
  Quality Sequence: trace file contained 17 contiguous distinct peaks
  following vector sequence.
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    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_7"
    /note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:
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    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
  source

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Query Match      0.2%; Score 12.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5403 AAAAAAGAAATGAA 5419
Db 17 AAAAAAAGAAATGAA 1

RESULT 816
CF297251/c
LOCUS
DEFINITION
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  30DGS--07-P12.g1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza
  sativa (japonica cultivar-group) cDNA clone 30DGS--07-P12, mRNA
  sequence.
ACCESSION
  CF297251
VERSION
  CF297251.1 GI:33666284
KEYWORDS
  EST.
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.

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REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
 COMMENT Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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RESULT 817 17 bp mRNA linear EST 15-AUG-2003  
 CF298341/c 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K24, mRNA  
 sequence.

ACCESSION CF298341 GI:33670102  
 VERSION CF298341  
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 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
 COMMENT Unpublished (2003)  
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